

From: Borin, Michael
Sent: Friday, September 09, 2005 4:23 PM
To: STIC-Biotech/ChemLib
Subject: Search request: 10617217

Examiner: M.Borin
AU: 1631
Mailbox: 2C70
Office: Remsen 2A55
Tel.: 20713

RE: 10617217; EST

ME
Please search nucleic acid SEQ ID NO: 88.

Thank you

na 2717

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STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

Date completed: _____

Searcher: Beverly e 2528

Terminal time: _____

Elapsed time: _____

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
_____ Other CGN



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number 165349

TO: Michael Borin
Art Unit: 1631
Location: REM/2A55/2C70
Serial Number: 10/617217

Friday, September 23, 2005

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

Db 721 CACAGTAAAGAAATTTTTCAGAGAGCTGTGTATTAAGACAAACATATATAGAAAG 780
 Oy 781 AGACAAAGAAATATGTATCAAGAAATTTATTCCTGAGAGAAACATATATATAGAGC 840
 Db 781 AGACAAAGAAATATGTATCAAGAAATTTATTCCTGAGAGAAACATATATATAGAGC 840
 Oy 841 TGGCTCTGTGTATTAAGAAATATATATATATATATATATATATATATATATATAT 900
 Db 841 TGGCTCTGTGTATTAAGAAATATATATATATATATATATATATATATATATATAT 900
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RESULT 5
 US-09-768-826-15
 ; Sequence 15, Application 09/768826
 ; Patent 09/020012966A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shi et al.
 ; TITLE OF INVENTION: 18 human secreted proteins
 ; FILE REFERENCE: PFS12P1
 ; CURRENT APPLICATION NUMBER: US/09/768, 826
 ; CURRENT FILING DATE: 2001-01-25

PRIOR APPLICATION NUMBER: PCT/US00/22350
 PRIOR FILING DATE: 2000-08-15
 PRIOR APPLICATION NUMBER: 60/148,759
 PRIOR FILING DATE: 1999-08-16
 NUMBER OF SEQ ID NOS: 61
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 15
 LENGTH: 1860
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-768-826-15

Query Match 67.6%; Score 1835.8; DB 9; Length 1860;
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DB 1822 ATAGTTGCAAGAGCTTTATATGCTTTATTAATGAAG 1860

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RESULT 6
 US-10-874-484-15
 Sequence 15, Application US/10874484
 Publication No. US20040235113A1
 GENERAL INFORMATION:

Bovin, M.
10/6/7217
Seq ID 88

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: September 22, 2005, 23:45:41; Search time 11587 Seconds
(without alignments)
11362.115 Million cell updates/sec

Title: US-10-617-217a-88

Perfect score: 2717
Sequence: 1 aaagaagaacagaaagcc.....ataaagctttattcttc 2717

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_hcg.*
3: gb_in.*
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5: gb_ov.*
6: gb_ov.*
7: gb_pl.*
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10: gb_ro.*
11: gb_srs.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	2666	98.1	147140	2	AC010226
6	2661	98.0	155276	2	AC091992
7	2546	93.7	3335	9	AY304584
8	2267	83.5	2637	9	AB055258
9	981	36.1	1149	9	AY275836
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C	25	467.6	17.2	880	10	AB100441	AB100441	AB100441
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ALIGNMENTS

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ACCESSION BD170656
VERSION BD170656.1 GI:27876468
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2717)
Matsuda, A., Honda, G., Muramatsu, S. and Nagano, Y.
NF-kappa B activation gene
Patent: WO 02053737-A 44-11-JUL-2002;
JOURNAL ASahi Kasei Corp, AKIO MATSUDA, GOICHI HONDA, SHUJI MURAMATSU, YUKIKO NAGANO
COMMENT OS Homo sapiens (human)
PN WO 02053737-A/44
PD 11-JUL-2002
PF 25-DEC-2001 WO 2001JP011389
PR 28-DEC-2000 JP 00P 402288, 26-MAR-2001 JP 01P 088912 PR
24-AUG-2001 JP 01P 254018
PI AKIO MATSUDA, GOICHI HONDA, SHUJI MURAMATSU, YUKIKO NAGANO
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A61K31/7088, A61K38/02, A61K39/395, A61K45/00, A61K48/00, A61P29/00, PC
A61P35/00
PC A61P37/00, C12Q1/68, C12N9/00, G01N33/15, G01N33/50, G01N33/53, PC
G01N33/57,
PC G01N33/68
CC NF-kappa B activation gene
FH Key location/Qualifiers
FT CDS location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

FEATURES

source
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AAAAGGAAACAGAAAAAGCCGGGCTGACTGTGTGGGCTCGCTGCAGATTGAAAAG 60
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RESULT 2
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 VERSION AB097022.1 GI:31455498
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 Matsuda, A., Suzuki, Y., Honda, G., Muramatsu, S., Mutsuzaki, O., Nagano, Y., Doi, T., Shimotohno, K., Harada, T., Nishida, E., Hayashi, H. and Sugano, S.
 Large-scale identification and characterization of human genes that activate NF-kappaB and MAPK signaling pathways
 Oncogene 22 (21), 3307-3318 (2003)

TITLE
 JOURNAL MEDLINE 12761501
 PUBMED 22646590
 REFERENCE
 2 (bases 1 to 2717)
 Matsuda, A., Suzuki, Y., Honda, G., Muramatsu, S., Mutsuzaki, O., Nagano, Y., Harada, T., Nishida, E., Hayashi, H. and Sugano, S.
 Direct Submission
 Submitted (25-NOV-2002) Yutaka Suzuki, The Institute of Medical Science, The University of Tokyo, Minatoku Shirokanedai 4-6-1, Tokyo, Tokyo 108-8639, Japan (E-mail: yusuzuki@ime.u-tokyo.ac.jp, Tel: 81-3-5449-5343, Fax: 81-3-5449-5416)
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VERSION AY304583.1 GI:37677664
KEYWORDS

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 REFERENCE 1 (bases 1 to 3453)
 AUTHORS Hardy, M.P., McGettrick, A.F., Eideback, M. and O'Neill, L.A.U.
 TITLE Identification of a novel variant of the Toll-like receptor adaptor protein TIRAP3
 JOURNAL 2 (bases 1 to 3453)
 REFERENCE Hardy, M.P., McGettrick, A.F. and O'Neill, L.A.U.
 AUTHORS Direct Submission
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 2039 AACATTTAGATGTTAAGCTGATGATCAATTAATCAAGAAATAGATGATGATGATG 2098
 1362 AACATTTTAAAGAACCCAGTCAATGATTTTCTGCTGAATCTGCAATTTTGAAGCA 1421
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 2159 TTTCACCAACCGATTCACAGCCCATTTGATAGTGTGTAGAGGACTTGGAGAGT 2218
 1482 GTGTTCAAGAGTCCCTGCGGCTTAAATCTTCAATTAATGATCAATTTTGAATG 1541
 2219 GTGTTCAAGAGTCCCTGCGGCTTAAATCTTCAATTAATGATCAATTTTGAATG 2278
 1542 CTTTATTTGACAGCTTTCTAATAAGCGGTATACCTGTGTAGTGGCCAGATATTCATTTT 1601

Db	2279	CTTTATTGGAGAGCTTCTTAAAGGCGTATACGTGTGAGTGGCAGATATTCATTTT	2338
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Db	2339	TAAATCAAAAACTCTCTTATGGAAGCTTTAAAGTTTCCGTACACACAAATTCCTCTCT	2398
Oy	1662	CAGGAAGATTTCTCATTTAGGCTCTCAAAGAGCTGACGTGTGCACTGTGTGTGTG	1721
Db	2399	CAGGAAGATTTCTCATTTAGGCTCTCAAAGAGCTGACGTGTGCACTGTGTGTGTG	2458
Oy	1722	ATAGGTTATTTATTAAGACTTTGATAGAGAAGATGATTTTATTTACCTCTCATTTCTAG	1781
Db	2459	ATAGGTTATTTATTAAGACTTTGATAGAGAAGATGATTTTATTTACCTCTCATTTCTAG	2518
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Db	2519	AGCCCAATGCTCTTAACAAGCCAGAGAGCCCAACAGAAATGTTCTTCCCTCCACAG	2578
Oy	1842	CCCTTCTGCCATCTGAGATTTAGGGAGCATCTGTCACTTGAAGATCAGGGATGGGGTGA	1901
Db	2579	CCCTTCTGCCATCTGAGATTTAGGGAGCATCTGTCACTTGAAGATCAGGGATGGGGTGA	2638
Oy	1902	GAAATGGTCATGTCAATGATAGAAAAAGCCCTCTTGGGATCATGACCTTGGTTCTAG	1961
Db	2639	GAAATGGTCATGTCAATGATAGAAAAAGCCCTCTTGGGATCATGACCTTGGTTCTAG	2698
Oy	1962	TCCAAATTCGTCCACTGAGGATGGAATGPACTGTGGGGCAAACTPAATTAACCTCCTTATC	2021
Db	2699	TCCAAATTCGTCCACTGAGGATGGAATGPACTGTGGGGCAAACTPAATTAACCTCCTTATC	2758
Oy	2022	TGTGAATGAAAGGGTGAATTTGATGATCTCTAAAGCTTTTGTCTCTATGAGATGT	2081
Db	2759	TGTGAATGAAAGGGTGAATTTGATGATCTCTAAAGCTTTTGTCTCTATGAGATGT	2818
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Db	2819	GAAAAATCAGGAGCACCAAAAAGGGAACAAGCAAAAAAGTTTGGATTCGATAAAGTAT	2878
Oy	2142	GTAATAGTTCAGAGAAGGCTTTATATATATGCTTATATGAAAGATTTTGTGTAATTA	2201
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Db	3059	CTTAAATTTCTTTTCTTATTTCCCACTGTATATCCCTACACAGTACCGGGATCTGCAC	3118
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Db	3119	ACATCTTTTTCAGATTAACCTCTTCAATAGCCATGAACAAACGTTCTATGAGAGCATGC	3178
Oy	2442	AAGTAAAGCAAGCCCTCAATCTGTGTAGTACTATTAAGAGAGAGATGTTTTCATTCG	2501
Db	3179	AAGTAAAGCAAGCCCTCAATCTGTGTAGTACTATTAAGAGAGAGATGTTTTCATTCG	3238
Oy	2502	ATAAGTACATTTTCTTACGCTTAAACGTTCTGATATAGTACTTACTACTTCTCTTTT	2561
Db	3239	ATAAGTACATTTTCTTACGCTTAAACGTTCTGATATAGTACTTACTACTCTCTCTTTT	3298
Oy	2562	CAGTTTTCATPATAAGTATCAATTTTTCGATTAAGCTTCCTGTAAAGCAATTTTAT	2621
Db	3299	CAGTTTTCATPATAAGTATCAATTTTTCGATTAAGCTTCCTGTAAAGCAATTTTAT	3358
Oy	2622	ATACTTAATTAACAATGAACGTGCCACTCTTCAATGCTTCGAAACTTGGGGCAATGTATGC	2681

DB		3359	ATACTAATTAATAACAGTGAACGTGGCACCATTTCATGSCCTGCAGAAACTGTGGCGCAATGTAGAC	3418
OY		2682	TAAATGCTATTTTTAAATAATTAATGTTTTATCTT	2716
Db		3419	TAAATGGATTTTTTAAATAATAATGTTTTATCTT	3453
RESULT 4				
ACCO8587/c				
LOCUS	ACCO8587	124310 bp	DNA	linear HTG 20-APR-2001
DEFINITION	Homo sapiens chromosome 5 clone CTC-570H22, WORKING DRAFT SEQUENCE.			
	23 unordered pieces.			
ACCESSION	ACCO8587			
VERSION	ACCO8587.5 GI:13699388			
KEYWORDS	HTG; HTGS_PHASEI; HTGS_DRAFT; HTGS_ACTIVEFIN.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 124310) DOE Joint Genome Institute. Sequencing of Human Chromosome 5 Unpublished			
AUTHORS	2 (bases 1 to 124310) DOE Joint Genome Institute. Direct Submission			
JOURNAL	Submitted (03-ANG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA			
REFERENCE	On Apr 20, 2001 this sequence version replaced gi:7708958.			
TITLE				
JOURNML				
COMMENT				

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Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

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Project Information
Center Project Name: 404250
Center clone name: CIT-HSPC_570H22
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Summary Statistics
Consensus quality: 108340 bases at least Q40
Consensus quality: 113349 bases at least Q30
Consensus quality: 114811 bases at least Q20
Estimated insert size: 204000; pulse field gel estimation
Estimated insert size: 122110; sum-of-coverage estimation
Quality coverage: 7.16 in Q20 bases; pulse field gel estimation
Quality coverage: 11.95 in Q20 bases; sum-of-coverage estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
1007 1006: contig of 1006 bp in length
1107 1106: gap of unknown length
2846 2846: contig of 1740 bp in length
2847 2846: gap of unknown length
4069 4069: contig of 1123 bp in length
4070 4169: gap of unknown length
4170 5211: contig of 1042 bp in length
5212 5311: gap of unknown length
5312 7256: contig of 1945 bp in length
7257 7356: gap of unknown length
7357 8963: contig of 1607 bp in length
8964 9063: gap of unknown length
9064 10487: contig of 1424 bp in length
10488 10587: gap of unknown length
10588 14221: contig of 3634 bp in length
14222 14321: gap of unknown length
14322 16089: contig of 1766 bp in length
16090 16189: gap of unknown length
16190 18580: contig of 2391 bp in length

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Db	91950	AGA CAGCA TTTACAGAA TTTGATGATGCTGTAAATGGGTCGTGACATCTTAATTA	92009
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OY	705	AGTCGTGGAATTTCTCA CACAGATGAGAAAGAAATTTTCA GAGTCGTGTATTA GACAA	764
Db	92190	AGTCGTGGAATTTCTCA CACAGATGAGAAAGAAATTTTCA GAGTCGTGTATTA GACAA	92249
OY	765	CAAACTATATGGAAGAAGACACAGAAATATGTATCAAAAGACAATTTATTTGCTGAGATGA	824
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OY	825	ACATATATACATGTGTGGCTGCTCTGTTTGTAAACCAATGATTAATCTTCACTTGAGAA	884
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OY	885	AGCAGTTTCTAGAAATGTTTAAATAAAGAGTCTTCACTTAAAGAAACCTATGAG	944
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OY	945	CACAAAGAAAGATAATTTCTGCGAGACAGCCTTAATAATTTGTGTACTTTTGAATCTTC	1004
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OY	1005	AGTAAACTTTCGACTTGTCA GAGTTCAAGACCTTTCTTCA CAATTTCTGATGTCATG	1064
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OY	1065	GATATGAAAAAGAAATCTCAATCATATTTCTTGTATTTGAACCTTGAACAAAACTTGT	1124
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OY	1305	ATTATGACATGTTAAAGCTGTATGCA TTTAAATCAGAAATATGATGAGAAATGGTGAAC	1364
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Db	93030	TATTTGCAGAGCTTCTAAAAGCGTAACTGTGTGTAGTGGCCAGATATTCATTTTTCAG	93089
QY	1605	ATCAAAAACCTCTCTTAATGGAAGCTTAAAGTTTCCGTCAACACAAATCTCTTCTCAG	1664
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QY	2445	TAAAGCAAGCCCTCAATCTGTAGTAACTTATAGAGAGGAATGGTTTTCATTCGATA	2504
Db	93930	TAAAGCAAGCCCTCAATCTGTAGTAACTTATAGAGAGGAATGGTTTTCATTCGATA	93989
QY	2505	GTGACATTTTCTTACCTTAAAGGTTCTGATAGTACCTTACTCATCTTCTTTTCAG	2564

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AC091992 155276 bp DNA linear HTG 31-AUG-2001
LOCUS Homo sapiens chromosome 5 clone RP11-90P14, WORKING DRAFT SEQUENCE,
DEFINITION 6 unordered pieces.
AC091992
AC091992 GI:15290436
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 155276)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
2 (bases 1 to 155276)
DOE Joint Genome Institute.
Direct Submission
Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Aug 25, 2001 this sequence version replaced gi:14333928.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 441299
Center clone name: RPCR-11_90P14

Summary Statistics
Consensus quality: 151184 bases at least Q40
Consensus quality: 153297 bases at least Q30
Consensus quality: 153815 bases at least Q20
Estimated insert size: 159350; agarose-fp estimation
Estimated insert size: 154776; sum-of-coverage estimation
Quality coverage: 5.9 in Q20 bases; agarose-fp estimation
Quality coverage: 6.07 in Q20 bases; sum-of-coverage estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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7460 17306: gap of unknown length
7460 17306: contig of 9847 bp in length
17307 17406: gap of unknown length
17407 37466: contig of 20060 bp in length
37467 37566: gap of unknown length
37567 57351: contig of 19785 bp in length
57352 57451: gap of unknown length
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/chromosome="5"
/clone="RP11-90P14"
/clone_lib="RPCR human BAC library 11"
ORIGIN
Query Match 98.0%; Score 2661.8; DB 2; Length 155276;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2666; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 45 CCGGAGATTTGAAAGAAATGCTGGAATCATATAGTTTCCCTCTGCTGGATA 104
Db 43524 CTTTATGATGAAAGAAATGCTGGAATCATATAGTTTCCCTCTGCTGGATA 43583
Qy 105 TTTATTAATGGGATCGGGAAGCTTAAATTAATTCCTGCTTCTCTTGGGGT 164
Db 43584 TTTATTAATGGGATCGGGAAGCTTAAATTAATTCCTGCTTCTCTTGGGGT 43643
Qy 165 AAAAGGCAAGTGTGGATCAAGTCCAGGATTCATGAGTCAGATTCCAGAAAGTCTGA 224
Db 43644 AAAAGGCAAGTGTGGATCAAGTCCAGGATTCATGAGTCAGATTCCAGAAAGTCTGA 43703
Qy 225 GATCTATGCTTGTGTAATGTTGCTGAGCAGCAATACAGAGGGGCAAGAGAAAG 284
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Db 43764 CAGAGGAGAGCTCAGAGCGTGGAGAGATGTTTGAAGAAAGCTGAAGAAAGGTGTC 43823
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 Db 44484 AGTAACTTGACATGTGTGAGATTTCAAGACCTTTCTTTTCAAAATTTTCTAGTTCAAG 44543
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 Db 44544 GATATGAAAAGAAATTTCTCAATCCATGTTTGAATGAACTTGAACAAAACCTGTG 44603
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 Db 44604 ATGACAGACATTTTAAATATGACAAACATTTTATCTGTGAATTTGTATCTCAAG 44663
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RESULT 7
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 ACCESSION AY304584
 VERSION AY304584.1 GI:37677666
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCES
 1 (bases 1 to 3335)
 Hardy,M.P., McGettrick,A.F., Bjedack,M. and O'Neill,L.A.J.
 Identification of a novel variant of the Toll-like receptor adaptor
 protein TIRAP3
 JOURNAL Unpublished
 2 (bases 1 to 3335)
 Hardy,M.P., McGettrick,A.F. and O'Neill,L.A.J.
 Direct Submision
 JOURNAL Submitted (23-MAY-2003) Biochemistry, Trinity College Dublin,
 College Green, Dublin 2, Ireland
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ORIGIN

Query Match      93.7%; Score 2546.4; DB 9; Length 3335;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2547; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY    289  AGGAGCTCAGAGCGTGAAGAGATGTTGAAGAAGCTGAAGAAGGTGTTCTCA 348
Db    289  AGGAGCTCAGAGCGTGAAGAGATGTTGAAGAAGCTGAAGAAGGTGTTCTCA 967
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Db    349  AATTGTGATATTGCATGACAGAGATGTTGAAGAAGAGCTGAAGAAGAGGTGTTCTCA 1027
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DEFINITION
ACCESSION AB055258
VERSION AB055258.1 GI:12698110
KEYWORDS
SOURCE Macaca fascicularis (crab-eating macaque)
ORGANISM Macaca fascicularis
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE
AUTHORS Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M.,
Tero,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
TITLE Isolation of full-length cDNA clones from macaque brain cDNA
libraries
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2637)
AUTHORS Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
TITLE Direct Submission
SUBMITTED (02-FEB-2001) Katsuyuki Hashimoto, National Institute of
Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
(E-mail:hashim@nih.go.jp, URL:http://www.nih.go.jp/yoken/genbank/,
Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
COMMENT
Lab host: TOP10
Vector: pME18S-FL3 (Acc.No. AB009864)
R. Site1: DraIII (CACTGCTG)
R. Site2: DraIII (CACCATGTG)
Description: 1st strand cDNA was primed with an oligo(dT) primer
[ATGAGCCTTTTCTTTTCTTTT]; double-stranded cDNA was synthesized
using specific 5' and 3' primers and amplified by PCR. The PCR
product was digested with SfiI and size selection was performed to
exclude fragments <1.5kb. The SfiI-digested PCR product was cloned
into distinct DraIII sites of pME18S-FL3. XhoI sites just outside
the DraIII sites can be used to isolate the cDNA insert. Libraries
were constructed by Sugano et al. (University of Tokyo, Institute of
Medical Science). Custom primer used for sequencing
( 5' end primer [CTTGTGCTTAAAGCTGCG] ;
3' end primer [GAGCTGAGCTGAGACAC] ).
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Db 1834 ACTCTTC--GATCATGAGACTGTGTTCTAGTCCAAATCTGCACTGAGAGTGAATGTA 1891
Qy 1992 CTGTGGGCAAACTATTTTACCTCTCTTATCTGTGAATGAAGGTTGAATTTGATGATC 2051
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				AY275836.1	GI:32435942	

REFERENCE	1 (bases 1 to 1149)
AUTHORS	Bin, L.-H., Xu, L.-G. and Shu, H.-B.
TITLE	TIRP, a Novel Toll/interleukin-1 receptor (TIR) Domain-containing Adapter Protein Involved in TIR Signaling
JOURNAL	J. Biol. Chem. 278 (27), 24526-24532 (2003)
MEDLINE	22716271
PUBMED	12721283
REFERENCE	2 (bases 1 to 1149)
AUTHORS	Bin, L.-H., Xu, L.-G. and Shu, H.-B.
TITLE	Direct Submission
JOURNAL	Submitted (14-APR-2003) Immunology, National Jewish Medical and Research Center, 1400 Jackson Street, K516c, Denver, CO 80206, USA
FEATURES	Location/Qualifiers
source	1..1149

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QY	222	GAAGATCTATCTTGTGTAAATGTGTGCGACAAGCATATACAAGAGGGCCCAACAGA	281
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Db	386	AAGCAGAGGAGACTCGAGCGTGAAGAGATTTTGAAGAAAGACTGAAGAGAGTG	445
QY	342	TTCTCAAAATTTGTGATATTTGACAGCAAGATGACAGATGAAGCCCTCAGAGTCCAG	401
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QY	402	AATCTGTATCAAGATGACTTTGGTATCAAAACCCGGAATATCTTTGCTGAGATGCCATGT	461
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QY	462	GGCAGACAGCACTTACAGATTTAGATGATGCTGTAATGGGCTGSCATGGAACAATCTTA	521
Db	566	GGCAGACAGCACTTACAGATTTAGATGATGCTGTAATGGGCTGSCATGGAACAATCTTA	625
QY	522	TTACTGACTGAAAACTTTTAAAGATGACTTGGTGTATATTTCCAGTTCTATAGTCCCTA	581
Db	626	TTACTGACTGAAAACTTTTAAAGATGACTTGGTGTATATTTCCAGTTCTATAGTCCCTA	685
QY	582	ATGAATCTCCGTAAcAGGCAAGCAATAATCACTCTGTATATACCATGCGGCCCTCGAAC	641
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DEFINITION	Sequence 3459 from Patent EP1386543.						
ACCESSION	CQ783319						
VERSION	CQ783319.1	GI:45503249					
KEYWORDS	.						
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

1 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Makamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
Primers for synthesizing full length cDNA clones and their use
Patent: EP 1396543-A 3459 10-MAR-2004;
Research Association for Biotechnology (JP)
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ORIGIN

Query Match 32.4%; Score 880.6; DB 6; Length 1687;
Best Local Similarity 99.5%; Pred. No. 5.2e-171;
Matches 883; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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801 TGGCCTATTGATTGAAAAAGAAATGCTGAGAAATACATAAAGTTTCCTCTTGGCTTGG 860
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Qy 981 GAAAGTCTATCTCTTGTGTAATGTTGCTGAGCAAGCAATACAAAGAGGGGCAACAGA 1040
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Db 702 GAAAGTCTGATTTCTTACACAAAGTGAAGAAATTTTTCAGAGAGTCTGTGTATTAAGACA 761

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RESULT 11
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LOCUS BD127586 1687 bp DNA linear PAT 18-SEP-2002
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD127586
VERSION BD127586.1 GI:23222531
KEYWORDS JP 2002017375-A/3017.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1687)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Makamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
Primers for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 3017 22-JAN-2002;
JOURNAL HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002017375-A/3017
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
PI ISHII,
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUOT OTSUKI, HISASHI KOGA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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Primer for synthesizing full-length cDNA and use thereof PH Key

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Query Match 32.4%; Score 880.6; DB 6; Length 1687;
Best Local Similarity 99.5%; Pred. No. 5.2e-171;
Matches 883; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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LOCUS AK075218
DEFINITION Homo sapiens cDNA FLJ90737 f18, clone PLACE1010827, weakly similar
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ACCESSION AK075218
VERSION AK075218.1 GI:22761164
KEYWORDS oligo capping; f18 (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

```

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REFERENCE
AUTHORS Isegai,T., Oca,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
        Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,
        Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
        Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.,
        Aoebuka,S., Sasaki,N., Hatcori,A., Okumura,K., Iwayanagi,T. and
        Nihoiye,K.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1687)
AUTHORS Isegai,T. and Otsuki,T.
TITLE Direct Submission

```

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JOURNAL
Submitted (25-MAR-2002) Takao Isegai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomicehri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).
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ORIGIN
Query Match 32.4%; Score 880.6; DB 9; Length 1687;
Best Local Similarity 99.5%; Pred. No. 5,2e-171;
Matches 883; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 42 TCGCTGCAAGTTGAGAAAGAAATGCTGAGAAATACATTAAGTTTCCTTCTGCTTGG 101
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Db 801 TGGCCTATGTGATGAGAAAGAAATGCTGAGAAATACATTAAGTTTCCTTCTGCTTGG 860
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Db 1641 GAAAGCATTTTCTAGAGAAATGTTTAAATAAAGAGTCTTCACTT 1687

RESULT 13
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LOCUS Homo sapiens TICAM-2 mRNA for TIR-containing adapter molecule-2,
DEFINITION complete cds.
ACCESSION ABI09098
VERSION ABI09098.1 GI:37360901
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
AUTHORS Oshiumi, H., Sasaki, M., Shida, K., Fujita, T., Matsumoto, M. and Seya, T.
TITLE TICAM-2: a bridging adapter recruiting to Toll-like receptor 4
JOURNAL J. Biol. Chem. (2003) In press
2. (bases 1 to 808)
Oshiumi, H., Shida, K., Matsumoto, M. and Seya, T.
Direct Submision
Submitted (22-APR-2003) Hiroyuki Oshiumi, Osaka University,
Department of Biology, Graduate School of Science, Machikaneyama
1-1, Toyonaka, Osaka 560-0043, Japan
(E-mail: oshiumi@bio.sci.osaka-u.ac.jp, Tel: 81-6-6850-5432,
Fax: 81-6-6850-5440)

FEATURES
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1. .808
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Best local Similarity 100.0%; Pred. No. 5.3e-156;
Matches 808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 265 CAGAGGGGCAACAGAAAGCAGAGGGAGCTCAGAGGCTGGAAGAGATGTTGAAGAG 324
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Db 241 CAGAGGGGCAACAGAAAGCAGAGGGAGCTCAGAGGCTGGAAGAGATGTTGAAGAG 300
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DEFINITION
ACCESSION AB091054
VERSION AB091054.1 GI:37360705
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
AUTHORS Oshiumi, H., Sasaki, M., Shida, K., Fujita, T., Matsumoto, M. and Seya, T.
TITLE TIR-containing Adapter Molecule (TICAM)-2, a Bridging Adapter
Recruiting to Toll-like Receptor 4 TICAM-1 That Induces
Interferon-{beta}
JOURNAL J. Biol. Chem. 278 (50), 49751-49762 (2003)

PUBMED 14519765
 2 (bases 1 to 725)
 Oshiumi, H., Shida, K., Matsumoto, M. and Seya, T.
 AUTHORS
 TITLE
 JOURNAL

Submitted (28-AUG-2002) Hiroyuki Oshiumi, Osaka Medical Center for
 Cancer and Cardiovascular Diseases, Department of Immunology, 1-3-3
 Nakamichi, Higashinari-Ku, Osaka, Osaka 537-0025, Japan
 (E-mail: oshiumi@bio.sci.osaka-u.ac.jp, Tel: 81-6-6973-1209,
 Fax: 81-6-6973-1209)

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 location/Qualifiers

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 Best Local Similarity 100.0%; Pred. No. 6.7e-139;
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 Db 61 AGGCAAGTGTGATGATACAAAGTCAGAGATATCATGATGATTCAGAAAGCTGAAT 120
 QY 228 CTATCTCTTGTGTAATGTGTCTGAGCAGCAATACAGAGAGGCGCAACAGAAAGCAG 287
 Db 121 CTATCTCTTGTGTAATGTGTCTGAGCAGCAATACAGAGAGGCGCAACAGAAAGCAG 180
 QY 288 GAGGAGCTCAGAGCGTGGAGAGATGTTTGAAGAAGAGCTGAAGAGAGGTTCTTC 347
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 QY 348 AAATTTGTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 407
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 QY 408 CTACAGATGATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 467
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 QY 468 CAGCATTTACAGAAATTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 527
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 QY 528 ACTGAAAATCTTTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 587
 Db 421 ACTGAAAATCTTTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 QY 588 TCCGTTAAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 647
 Db 481 TCCGTTAAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 QY 648 CTTCCCGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 707
 Db 541 CTTCCCGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600

QY 708 CGTGATTTCTTACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 767
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 Db 661 ACTATATGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 QY 828 TATTA 832
 Db 721 TATTA 725

RESULT 15
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 ACCESSION
 VERSION
 KEYWORDS
 ORGANISM
 SOURCE
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 708)
 Fitzgerald, K.A., Rowe, D.C., Barnes, B.J., Caffrey, D.R., Viscintin, A.,
 Latz, B., Monke, B., Piltha, P.M. and Goldenfleck, D.T.
 LPS-TLR4 Signaling to IRF-3/7 and NF- κ B Involves the Toll
 Adapters TRAM and TRIF

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBMED
 14517278
 2 (bases 1 to 708)
 Fitzgerald, K.A., Rowe, D., Barnes, B., Caffrey, D.R., Latz, B.,
 Monke, B., Piltha, P. and Goldenfleck, D.T.
 TRIF and TRAM: TLR adapter molecules regulating distinct pathways
 to IRF-3

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Submitted (09-FEB-2003). Infectious Disease & Immunology, University
 of Massachusetts Medical School, 366, Plantation Street, Lazare
 Research Building, Worcester, MA 01605, USA

FEATURES
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ORIGIN

Query Match 26.1%; Score 708; DB 9; Length 708;
 Best Local Similarity 100.0%; Pred. No. 2.2e-135;
 Matches 708; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: September 23, 2005, 01:29:31 ; Search time 8585 Seconds
(without alignments)
12046.665 Million cell updates/sec

Title: US-10-617-217a-88
2717
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2.*
3: gb_hc1.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gest1.*
9: gb_gest2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	733.2	27.0	1005 5	BX391740 BX391740
3	721.2	26.9	923 6	CD518425 AGENCOURT
4	727.4	26.8	753 7	CR737757 CR737757
5	715.4	26.3	728 6	CB529150 UI-H-ED0
6	707.4	26.0	710 5	BX112907 BX112907
7	663	24.4	681 6	CA440665 UI-H-ED0
8	662	24.4	707 6	CA438249 UI-H-ED0
9	648.2	23.9	887 5	BO438847 AGENCOURT
10	610	22.5	635 6	CA441688 UI-H-ED0
11	606.4	22.3	615 4	BI493312 dfe9906.y
12	602.8	22.2	613 4	BI493311 dfe9906.w
13	567.8	20.9	585 6	CD638761 AGENCOURT
14	554.8	20.4	560 8	AQ319961 RPT111-11
15	533	19.6	533 2	BE502913 h281B01.x
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17	520	19.1	520 4	BM624561 K-EST0096
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20	492.6	18.1	744 7	CN270023 170005999
21	481.8	17.7	498 2	AM450623 UI-H-B13
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23	467.6	17.2	481 1	AI423165 cf32d04.x
24	461.8	17.0	469 1	AI218114 qh27b07.x

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C 35	389	14.3	427 1	AI184915	AI184915	ok28a11.x
C 36	384.2	14.1	390 1	AI400110	AI400110	cg62b11.x
C 37	383.8	14.1	428 2	BP511084	BP511084	UI-H-B14
C 38	375	13.8	426 2	BF509113	BF509113	UI-H-B14
C 39	370	13.6	370 1	AI143515	AI143515	qa51G09.8
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ALIGNMENTS

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DEFINITION
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ACCESSION
BX391704
VERSION
BX391704.2 GI:46875240
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30619511.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by life technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
2860.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna7s=CS0BA1020ZG05_CS01863_1ec=2860.r

FEATURES

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/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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Query Match 31.0%; Score 841.2; DB 5; Length 904;
Best Local Similarity 97.7%; Pred. No. 3.6e-185;
Matches 874; Conservative 0; Mismatches 19; Indels 2; Gaps 2;

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 QY 1816 AACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1870
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RESULT 2
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 ACCESSION BX397140
 VERSION BX397140.2 GI:46846453
 KEYWORDS EST.
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 1 (bases 1 to 1005)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 13, 2003 this sequence version replaced gi:30613315.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
 end enriched, double-strand cDNA was digested with NotI and cloned
 into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 2860.x
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna78=CS0D1030MD06NP16c=2860.r.

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 /note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Query Match 27.0%; Score 733.2; DB 5; Length 1005;
 Best Local Similarity 78.9%; Pred. No. 160;
 Matches 786; Conservative 73; Mismatches 133; Indels 4; Gaps 2;

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 DB GAGGCCCAACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 817
 QY 1867 GAGCATGCTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1926
 DB GAGCATGCTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 757
 QY 1927 AAAGCCCTCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1986
 DB AAAGCCCTCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 697
 QY 1987 TGTAACTGTGGCAAACTATTAACCTCTTATCTGTGAAAATGAAGGGTTGAATTGAT 2046
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 QY 2167 ATGCTTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2226
 DB ATGCTTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 457
 QY 2227 CATTAACCTTAAGTACAGAGAAAAAATATATCATGCTTACAGGCTTTCTTAAAAAAT 2286

DG

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Oy	2347	ACTTGTAATCCCCCTCAACGATACGGGAGCTGCACAACATCTTTTTGCAGTTACCTTTCA	2408
Db	336	ACGGGGAATGSCSCCAACCAGKACCGGGATCCGCACACGSGktttYGGCGKTAACCTTTCA	277
Oy	2407	TAGCCATAAACCAAACGTTCTCATAGAGAGCATGCAATTAAGTCAAGCGCTCTTAATTCGT	2466
Db	276	TAGCCAKAAACCAAAACGGKCATATGGSGAGGSAAGAAAGGCKARGSTSTGTGTCGG	217
Oy	2467	TAGTACTATTAGAGAGAGAGATGTTTTTCATTGCATGTGACATTTTCTTAGCCTTAAC	2526
Db	216	KRGASKAAGTRGRRGRRGRRGAGGsktgGcATGSAKRKGKASMAAGGStTAgCCTTRAS	157
Oy	2527	GTTCTGATAGTAGCTTACTACTACTCTCTTTTCAGTTTTCATTAATAGATTCATTT	2586
Db	156	GKTCTGATAGRGTCTTACGACGCACTTCTCKTTTKCAGANGCANPAANAANNCATTG	97
Oy	2587	TTTGGCCATANTGCTTCTGTAAAGCCAAATTTTATATCTAATAAAAATGAATCGCCCA	2646
Db	96	NNNNGCCNNAAGGCMCMCMMAAAACCAATTTTATATCTAATAAAACTGAATCGCCCA	37
Oy	2647	CTCTTCATGCTGACCAACTTGGGGCAATTTGATGCT	2682
Db	36	CTCTTCATGCTGACCAACTTGGGGCAATTTGATGCT	1

LOCUS	CD518425	923 bp	mRNA	linear	EST 06-JUN-2003
DEFINITION	AGENCOURT 14374815 NIH-MGC_181 Homo sapiens cDNA clone IMAGE:30399931 5', mRNA sequence.				
ACCESSION	CD518425				
VERSION	CD518425.1	GI:31450143			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	1 (bases 1 to 923)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999)				
	Contact: Daniela S. Gerhard, Ph.D.				
	Office of Cancer Genomics				
	National Cancer Institute / NIH				
	Bldg. 31 Rm10A07 Bethesda, MD 20892				
	Email: csgrahb-remail.nih.gov				
	Tissue Procurement: Dr. Michael Brownstein				
	cDNA Library Preparation: Invitrogen Corp				
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)				
	DNA Sequencing by: Agencourt Bioscience Corporation				
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov				
	Plate: NDAM487	row: d	column: 20		
	High quality sequence start: 26				
	High quality sequence stop: 679.				

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FEATURES
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        Location/Qualifiers
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/note="Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV (destroyed); Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.42 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."

Query Match	26.9%	Score 731.2;	DB 6;	length 923;
Best Local Similarity	94.9%;	Pred. No. 1.7e-159;		
Matches 822;	Conservative 0;	Mismatches 33;	Indels 11;	Gaps 6

OY	1287	GAATTCGCAGAAATGGAACATTAGCATGTAAAGCGTAAATGCAATATAATCAGAAATAG	134
Db	21	GAATTCCTCGGAGATGAACATTAGCATTTTAAGCGTTAGATGCAATATAATCAGAAATAG	80
OY	1347	ATGTGAGAAATGTGTGAACCTTTTAAAGAAACCCAGTCAAAATGATATTTCTGCTGAAATCT	140
Db	81	ATGTGAGAAATGTGTGAACCTTTTAAAGAAACCCAGTCAAAATGATATTTCTGCTGAAATCT	140
OY	1407	GCATATTATTGAGGAGATTTCCACACGATTTACACAGCCCATTTGATGATGTGTAG	146
Db	141	GCAATTTTGGAGGCAATTTCCACACGATTTACACAGCCCATTTGATGATGTGTAG	200
OY	1467	GGACTTCGTGAGTGTGTTCAGACGTCCCTCGGGCTTAAATCTCTTCATATTTAGTCAT	152
Db	201	GGACTTCGTGAGTGTGTTCAGACGTCCCTCGGGCTTAAATCTCTTCATATTTAGTCAT	260
OY	1527	CATTGTGATCTATGCGCTTTATTTCCAGAGCTTTTAAAGGGGTATATCTGTGTAGTGC	158
Db	261	CATTGTGATCTATGCGCTTTATTTCCAGAGCTTTTAAAGGGGTATATCTGTGTAGTGC	320
OY	1587	CAGATATTCACTTTTATAGATCAAAAACCTCTCTTTATGAGGCTTTTAAAGTTTCCGTAC	164
Db	321	CAGATATTCACTTTTATAGATCAAAAACCTCTCTTATGAGGCTTTTAAAGTTTCCGTAC	380
OY	1647	ACACAATTCCTCTTCAGGAAGATTTTCATTTAGTCTTCAAGTACCTGACTGTGT	170
Db	381	ACACAATTCCTCTTCAGGAAGATTTTCATTTAGTCTTCAAGTACCTGACTGTGT	440
OY	1707	GCATGTGTGTGTGATATGTTATTTTAAAGACTTTGATAGAGAGATGATATTTAT	176
Db	441	GCATGTGTGTGTGATATGTTATTTTAAAGACTTTGATAGAGAGATGATATTTAT	500
OY	1767	TACCTCCTATTCTAGAGGCCCATGCTCCTTAACAAGCCAGAGGCCCCAACAAGATTGT	182
Db	501	TACCTCCTATTCTAGAGGCCCATGCTCCTTAACAAGCCAGAGGCCCCAACAAGATTGT	560
OY	1827	TTCTTTCTCCACAGCCCTTCTGCCCATCTGAGATTGAGGAGCATCTGCCATTGAGAT	188
Db	561	TTCTTTCTCCACAGCCCTTCTGCCCATCTGAGATTGAGGAGCATCTGCCATTGAGAT	620
OY	1887	CAGGGAATGGGTGAGAAATGGGTATATGCAATGATAAGAAAGGCCCTTGGGGATCAT	194
Db	621	CAGGGAATGGGTGAGAAATGGGTATATGCAATGATAAGAAAGGCCCTTGGGGATCAT	680
OY	1947	GAGACTTGATCTAGTCCAAATTTCTGCACATGAGAGATGATGTAATCTGT--GGCAAACTA	200
Db	681	GAGACTTGATCTAGTCCAAATTTCTGCACATGAGAGATGATGTAATCTGTGGGGCAAACTA	740
OY	2006	TTTA--CCCTCCTTATCTGTGAAATGAAAGGTT--GAATTGATGATCTCTTAAAGGCT	206
Db	741	TTTATCCCTCCTTATCTGTGAAATGAAAGGTTGATGATGATGATCTCTTAAAGGCT	800
OY	2062	TTTGT--CCTCATAGAGATGTGAAAAA--CTAGGGACCACAAAAAGGAGCA--GCATA	211
Db	801	AATGTCCCTCATAGAGATGTGAAAAA--CTAGGGACCACAAAAAGGAGCA--GCATA	860
OY	2116	AAAGTTTGATTCGATTAAGTATAT	2141
Db	861	AAAGTTTGATTCGATTAAGTATAT	886

	CR737757	753 bp	mRNA	linear	EST 27-AUG-2006
LOCUS	CR737757				
DEFINITION	CR737757 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE971D037 ; IMAGE:132835 5', mRNA sequence.				
ACCESSION	CR737757				
VERSION	CR737757.1				
KEYWORDS	GI:51587215				
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 753) Ebert, L., Hell, O., Hennig, S., Korn, B., Neubert, P., Partech, B., Peters, M., Radelof, U. and Schneider, D. I. M.A.G.E. cDNA Clone Collection Unpublished (2004)				
TITLE	JOURNAL				
COMMENT	Contact: Inge Ariart RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Email: www.rzpd.de RZPD: IMAGE971D037. RZPDLIB: I.M.A.G.E. cDNA clone collection; Contact: Inge Ariart RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel.: +49 30 32639 100 Fax: +49 30 32639 111 www.rzpd.de This clone is available royalty-free from RZPD: contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, primer sequence: TTTCACACAGGAACAGCTATGAC. Location/Qualifiers 1..753 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE971D037 ; IMAGE:132835" /sex="female" /dev_stage="placenta obtained at birth (full term)" /lab_host="DH10B (ampicillin resistant)" /clone_1lb="Soares placenta Nb2HP" /note="Organ: placenta; Vector: pTRIP3 (Pharmacia) with a modified polylinker; Site 1: Not I, Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAGAATTGGCGGCCGCAGGAATTTTTTTTCTTTT 3'] , double-stranded cDNA was ligated to Eco RI adaptore (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTRIP3 vector. Library went through one round of normalization. library constructed by Bento Soares and M.Patima Bonaldo."				
ORIGIN					
Query Match	26.8%; Score 727.4; DB 7; Length 753;				
Best Local Similarity	99.6%; Pred. No. 1.3e-158;				
Matches 750; Conservative	0; Mismatches 1; Indels 2; Gaps 2;				
Oy	1206 AGAAGATCTTGATCACACTTCCTCCGTGAGGCACTCTCATAGATGTTGCATTAAGCATTCG	1265			
Db	1 AGGAATCTTGATGACACTTCCTCCGTGAGGCACTCTCATAGATGTTGCATTAAGCATTCG	60			
Oy	1266 GGTACTATCACCACAATAATATGAATTGCGAGAAATGAACATTAGCATGTTAAGCGTTGA	1325			
Db	61 GGTACTATCACCACAATAATATGAATTGCGAGAAATGAACATTAGCATGTTAAGCGTTGA	120			
Oy	1326 TGCATATTAATAATCAGAAAATAGATGTGAGATGTCGAACTTTTAAAAAACCCAGTCGA	1385			
Db	121 TGCAATATAAAATCAGAAAATAGATGTGAGAAATGTCGAACTTTTAAAAAACCCAGTCGA	180			
Oy	1386 ATGATTTTTCGCTGAAAATTCGCAATTTTGGAGCAATTTCCACACACCGATTCAACAGCC	1445			
Db	181 ATGATTTTTCGCTGAAAATTCGCAATTTTGGAGCAATTTCCACACACCGATTCAACAGCC	240			
Oy	1446 ATTGAATAGTGTGATTTAGGACCTTCGTGAGATGTTGTTCAAGATCCCCCTGGGGCTT	1505			

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SOURCE	1. .753
	/organism="Homo sapiens"

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1. .753
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE971D037 ; IMAGE132835"
/sex="female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/clone_1lb="Scars placenta Nb2H"
/name="Organ; placenta; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AATCGAAGAATTGCGCGCGCGAATTATTTTATTTTATTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
was through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo. "

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Query Match	26.8%	Score 727.4	DB 7	Length 753
Best Local Similarity	99.6%	Pred. No. 1.3e-158		
Matches 750	Conservative	0	Mismatches 1	Indels 2
				Gaps 2

Oy	1266	GGTACTATCACCAGAAAATATGAATGGCCAGATAGAA	CATTTCAGCATGTTAAGCTTGA	1325
Oy	1266	AGAGAGATTCATCACTCCCTCCGAGGACCTCTCATGAT	GTGTGCATTAAGCATTTGG	1265
Db	1	AGGAGATTCGATCA	CACTTCCCTCCCTGAGGACCTCTCATGATGTTCATTAAGCATTTGG	60
Oy	1266	GGTACTATCACCAGAAAATATGAATGGCCAGATAGAA	CATTTCAGCATGTTAAGCTTGA	1325
Db	61	GGTACTATCACCAGAAAATATGAATGGCCAGATAGAA	CATTTCAGCATGTTAAGCTTGA	120
Oy	1336	TGCATATTAATTCAGAAAATAGATGTGACAA	TGCTGTGAACTTTTAAAGAACCCAGTCAA	1385
Db	121	TGCATATTAATTCAGAAAATAGATGTGACAA	TGCTGTGAACTTTTAAAGAACCCAGTCAA	180
Oy	1386	ATGTATTTTTCGCTGAAATATGTCATATTTTGAGAGCATTTCC	CAACCGATTCACAGGCC	1445
Db	181	ATGTATTTTTCGCTGAAATATGTCATATTTTGAGAGCATTTCC	CAACCGATTCACAGGCC	240
Oy	1446	ATTGTAGATGTGTGATTAGGACCTTCGTGAGTGCTGTTCAGACGT	CCCCCTGGGGCTTT	1505

Db	241	ATTGATATGCTGGTAGTTAGGACTTCGTGGAGTGGTGTTCAAGCGTCCCTGGGGCTT	300
OY	1506	AAATCTCTTCATATTAGTCATCAATTTGTAACTAAGCTTATATTTGCAGAGCTTCTAAAG	1567
Db	301	AAATCTCTTCATATTAGTCATCAATTTGTAACTAAGCTTATATTTGCAGAGCTTCTAAAG	360
OY	1566	GGGTAATACGTGTGAGAGTGGCCAGATATATCACTTTTATAGATCAAAAACCTGCTTAATGA	1625
Db	361	GGGTAATACGTGTGAGAGTGGCCAGATATATCACTTTTATAGATCAAAAACCTGCTTAATGA	420
OY	1626	AGCTTTAAAGTTCCTCGTCACACACAAATTCCTCTCAGGAAGTATTCGATTTAGGTC	1685
Db	421	AGCTTTAAAGTTCCTCGTCACACACAAATTCCTCTCAGGAAGTATTCGATTTAGGTC	480
OY	1686	TTCAAAGTAGCCTGACTGTGTGCATGTGTGTGTGATAGTTATTTATTAAGACTTTGG	1744
Db	481	TTCAAAGTAGCCTGACTGTGTGCATGTGTGTGTGATAGTTATTTATTAAGACTTTGG	540
OY	1746	ATAAAGAGATGATTTTATTACTCCATTTCTAGAGCCCAAGCCTCTTAACAAGCCAG	1805
Db	541	ATAAAGAGATGATTTTATTACTCCATTTCTAGAGCCCAAGCCTCTTAACAAGCCAG	600
OY	1806	AGAGGCCCAACA - GGAATGTTCTTCTCTCCACAGGCCCTTCTGCCATCTGAGATTGA	1864
Db	601	AGAGGCCCAACAAGGAGTGTCTTCTTCCCTCCACAGGCCCTTCTGCCATCTGAGATTGA	660
OY	1865	GGGAGCATCGTCCACTTGAGATCAAGGATGGGGTGGAGAAAT - GGGTCATGTCAATTAATG	1922
Db	661	GGGAGCATCGTCCACTTGAGATCAAGGATGGGGTGGAGAAATGGGGTCAATGTCAATTAATG	720
OY	1924	AGAAAGCCCTCTCGGAGATCATAGACTTGGT	1956
Db	721	AGAAAGCCCTCTCGGAGATCATAGACTTGGT	753

RESULT 5	
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LOCUS	728 bp mRNA linear EST 05-AUG-2004
DEFINITION	U1-H-PT2-bj-f-a-01-0-U1.s1 NCI CGAP_P72 Homo sapiens cDNA clone

ACCESSION	CB529150	
VERSION	CB529150.1	GI:29389547
KEYWORDS	EST.	
SOURCE	Homo sapiens	(human)
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS
TITLE

1 (bases 1 to 728)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgp>.
National Cancer Institute, Cancer Genome Anatomy Project (CCAP),

JOURNAL COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
E-mail: roberts@earthlink.net

Tissue Procurement: Dr. Gary W. Hunsinbake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
Seq primer: M13 FORWARD
POLYA=Yes.

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location/Qualifiers
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Db      121 TCCCACTGAGATTGAGGAGAGATGTCACCTTGATCAGGAGATGGGATGAATG 180
Qy      1908 GTCAATGTCAATGATGAGAAAGCCCTCTCCGGATCATGAGACTGTTCTAGTCAAT 1967
Db      181 GTCAATGTCAATGATGAGAAAGCCCTCTCCGGATCATGAGACTGTTCTAGTCAAT 240
Qy      1968 TTCTGCACTGAGATGAAATGTAATCTGTGGGCAAACTATTACCTCTTTATCTGTGA 2027
Db      241 TTCTGCACTGAGATGAAATGTAATCTGTGGGCAAACTATTACCTCTTTATCTGTGA 300
Qy      2028 ATGAAAGGGTTGAATGATGAGATCTCTAAAGGCTTTGCTCTATGAGAGATGAAAA 2087
Db      301 ATGAAAGGGTTGAATGATGAGATCTCTAAAGGCTTTGCTCTATGAGAGATGAAAA 360
Qy      2088 CTAGGAGCCACAAAGAGAAACAAGCAAAAGTTTGGATTGATAAGTATATATAT 2147
Db      361 CTAGGAGCCACAAAGAGAAACAAGCAAAAGTTTGGATTGATAAGTATATATATAT 420
Qy      2148 GTTGCAGAAAGGCTTTATATATGCTTTATATATGAAAAATATTTTGTATATGACAGAT 2207
Db      421 GTTGCAGAAAGGCTTTATATATGCTTTATATATGAAAAATATTTTGTATATGACAGAT 480
Qy      2208 AATTTATTTTATGCTGTCTATACCTTAAAGTCACAGAAAAAATATACAGCTTAC 2267
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RESULT 7
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LOCUS      CA440665      UI-H-ED0-axc-b-08-0-UI.61 NCI CGAP EDO Homo sapiens cDNA clone
DEFINITION      UI-H-ED0-axc-b-08-0-UI.61, mRNA sequence.
ACCESSION      CA440665
VERSION        CA440665.1 GI:24805085
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
Homosapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 681)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaab8-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-47, >AT richlow_complexity (matched complement)
Seq primer: M13 FORWARD
POLY(A)ies.
Location/Qualifiers

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ORIGIN

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/dev_stage="Adult"
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/clone_lib="NCI CGAP EDO"
/note="Organ: Left Pubic Bone; Vector: pT73-Pac
(Pharmacia) with a modified polylinker; Site 1: BclI I;
Site 2: Not I; NCI CGAP EDO is a cDNA library containing
the following tissue(s): Chondrosarcoma cell line C55. The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT73-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dr)18 tail. The sequence tag for this
library is GCTCAAGCT.
TAG_TISUB=chondrosarcoma
TAG_LIB=UI-H-ED0
TAG_SEQ=CTCAAGCT"

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Query Match 24.4%; Score 663; DB 6; Length 681;

Best Local Similarity 100.0%; Pred. No. 1,4e-143; Indels 0; Gaps 0;

Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2055 AAGGCTTTGCTCTATGAGATGTAAGAACTAGGAGCCACAAAGGAAACAGCA 2114
Db      681 AAGGCTTTGCTCTATGAGATGTAAGAACTAGGAGCCACAAAGGAAACAGCA 622
Qy      2115 AAAAGTTGATTCGATTAAGATGATGATGATGATGATGATGATGATGATGAT 2174
Db      621 AAAAGTTGATTCGATTAAGATGATGATGATGATGATGATGATGATGATGAT 562
Qy      2175 AATGAAAGATTTTGTATATGATGATGATGATGATGATGATGATGATGATGAT 2234
Db      561 AATGAAAGATTTTGTATATGATGATGATGATGATGATGATGATGATGATGAT 502
Qy      2235 TTAAGCTCAGGAAAAATATACATCTTACTGAGCTTCTTAAATATTTT 2294
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Qy      2295 TAGAGATCTTGAATGAAGACATTTTGTATATTTTCTTATTTCCCATTTGAT 2354
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Qy      2355 ATCCCTTACGATACCGGGATCTGACACATTTTTCAGTTACTGCTTACATGACAG 2414
Db      381 ATCCCTTACGATACCGGGATCTGACACATTTTTCAGTTACTGCTTACATGACAG 322
Qy      2415 AACCAAAAGCTTCTATGAGAGATGCAAGTAAAGCTCTTATCTGTAGTACT 2474
Db      321 AACCAAAAGCTTCTATGAGAGATGCAAGTAAAGCTCTTATCTGTAGTACT 262
Qy      2475 ATTAGAGAGAGATGATTTTCAATTCATATGATGATTTTCTTACCTTAAAGTTCTAT 2534
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Qy      2535 AGTAGCTTACTACTGATCTTCTTTTCAAGTTTCTATATATATATATATATATAT 2594
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Qy      2595 TAAATGCTTCTGTAAAGCAATTTTATATATATATATATATATATATATATAT 2654
Db      141 TAAATGCTTCTGTAAAGCAATTTTATATATATATATATATATATATATATAT 82
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Oy      2715 TTT 2717
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Db      21 TTT 19

RESULT 8
CA438249/c
LOCUS   707 bp  mRNA  linear  EST 08-NOV-2002
DEFINITION
  UT-H-DT1-avw-e-13-0-UI-s1 NCI_CGAP_DTI Homo sapiens cDNA clone
  UI-H-DT1-avw-e-13-0-UI 3', mRNA sequence.
ACCESSION
  CA438249
VERSION
  CA438249.1 GI:24802669
KEYWORDS
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SOURCE
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  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
  1 (bases 1 to 707)
  NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapb-remail.nih.gov
  Tissue Procurement: Dr. Jose Mercende
  cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Clone distribution information can be obtained
  from Dr. M. Bento Soares, bento-soares@iowa.edu
  The following repetitive elements were found in this cDNA
  sequence: 1-47, >AT-rich#low_complexity (matched compliment)
  Seq primer: M13 FORWARD
  POLYA=yes.

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    /clone_lib="NCI_CGAP_DTI"
    /note="Organ: Lung; Vector: pTTT3-Pac (Pharmacia) with a
    modified polylinker; Site 1: Ecor I; Site 2: Not I;
    NCI CGAP DT1 is a normalized cDNA library containing the
    following tissue(s): Metastatic Chondrosarcoma in Lung.
    The library was constructed according to Bonaldo, Lennon
    and Soares, Genome Research, 6:791-806, 1996. First strand
    cDNA synthesis was primed with an oligo-dT primer
    containing a Not I site. Double stranded cDNA was ligated
    to an Ecor I adaptor, digested with Not I, and cloned
    directionally into pTTT3-Pac vector. The oligonucleotide
    used to prime the synthesis of first-strand cDNA contains
    a library tag sequence that is located between the Not I
    site and the (dT)18 tail. The sequence tag for this
    library is AACTGTTCCG.
    TAG_TISSUE=Lung metastatic chondrosarcoma
    TAG_LIB=UI-H-DT1
    TAG_SEQ=AACTGTTCCG"

ORIGIN
  Query Match      24.4%; Score 662; DB 6; Length 707;
  Best Local Similarity 99.1%; Pred. No. 2,3e-143;
  Matches 676; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Oy      2096 CACAAAAGGAAACAAGAAAAAGTTGGATTGATTAAGTATGTAAATGTCAGA 2155
Db      640 CACAAAAGGAAACAAGAAAAAGTTGGATTGATTAAGTATGTAAATGTCAGA 581
Oy      2156 AGGCTTATATATGCTTATATATGAAAAAGATATTTTGTATATGACGCAATATTTATT 2215
Db      580 AGGCTTATATATGCTTATATATGAAAAAGATATTTTGTATATGACGCAATATTTATT 521
Oy      2216 TTTAATGCTGTCATTACCTTAAAGTCA CAGAAAAAAATATACATGCTGCTGAGGCTT 2275
Db      520 TTTAATGCTGTCATTACCTTAAAGTCA CAGAAAAAAATATACATGCTGCTGAGGCTT 461
Oy      2276 TCTTAAATAATTAATTTTATATAGATCCTTGAGTAAAGACATTTTGCTTAAATTTCTTTT 2335
Db      460 TCTTAAATAATTAATTTTATATAGATCCTTGAGTAAAGACATTTTGCTTAAATTTCTTTT 401
Oy      2336 TCTTATTTCCCACTTGATATATCCCTTACAGTACCAGGATTTGCACACATCTTTTGGAG 2395
Db      400 TCTTATTTCCCACTTGATATATCCCTTACAGTACCAGGATTTGCACACATCTTTTGGAG 341
Oy      2396 TTACCTGTCATAGCAATGAAACGAAAGCTTATAGAGAGATGCAAGTAAAGTCAAGCC 2455
Db      340 TTACCTGTCATAGCAATGAAACGAAAGCTTATAGAGAGATGCAAGTAAAGTCAAGCC 281
Oy      2456 TCTATTTCTGTACTACTTATTAAGAGAGAGATGTTTTCATTGACATAGTACATTTTC 2515
Db      280 TCTATTTCTGTACTACTTATTAAGAGAGAGATGTTTTCATTGACATAGTACATTTTC 221
Oy      2516 TTACCTTAAACGTTCTGATAGTACCTTACTACTGACTCTCTTTTCACTTTTCAATA 2575
Db      220 TTACCTTAAACGTTCTGATAGTACCTTACTACTGACTCTCTTTTCACTTTTCAATA 161
Oy      2576 AGATTCATTTTGTGCAATATGCTTCCTGTAAGCAATTTTATATACTAATTAACA 2635
Db      160 AGATTCATTTTGTGCAATATGCTTCCTGTAAGCAATTTTATATACTAATTAACA 101
Oy      2636 TGAATCGCCCACTGTCATAGCTGCGCAAACTTGCGGCAATGTGTAATGTATTTT 2695
Db      100 TGAATCGCCCACTGTCATAGCTGCGCAAACTTGCGGCAATGTGTAATGTATTTT 41
Oy      2696 AAAATAAATGTTTATTTCTTT 2717
Db      40 AAAATAAATGTTTATTTCTTT 19

RESULT 9
BQ438847
LOCUS   887 bp  mRNA  linear  EST 24-MAY-2002
DEFINITION
  AGENCOURT 7761668 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6018003
  5', mRNA sequence.
ACCESSION
  BQ438847
VERSION
  BQ438847.1 GI:21177923
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
  1 (bases 1 to 887)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapb-remail.nih.gov
  Tissue Procurement: ATCC
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LNL at:
  http://image.lnl.gov
  plate: LRAM3218 row: d column: 04
  High quality sequence stop: 664.

```

FEATURES
source

Location/Qualifiers
1..887
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6018003"
/tissue="epithelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="N1H MGC 70"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site: 1; NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.1 Kb. Library constructed by life technologies."

ORIGIN

Query Match 23.9%; Score 648.2; DB 5; Length 887;
Best Local Similarity 95.2%; Pred. No. 4,1e-140;
Matches 698; Conservative 0; Mismatches 32; Indels 3; Gaps 3;

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Qy 42 TCGCTGCGATTTGAAAAGAAATGCTGAAATATCATTAAGTTTCTCTTCTGCTTGG 101
Db 146 TGGCCTATTGATTTGAAAAGAAATGCTGAAATATCATTAAGTTTCTCTTCTGCTTGG 205
Qy 102 ATATTATTAATGGGTATCGGGAAGTCTTAATAATTTCTGCTCTTCTCTCTTGG 161
Db 206 ATATTATTAATGGGTATCGGGAAGTCTTAATAATTTCTGCTCTTCTCTCTTGG 265
Qy 162 GGTAAAGGCAAGGTGGAATCAAGTCAGAGTATCATAGTCAGATTCCAAAGAGCT 221
Db 266 GGTAAAGGCAAGGTGGAATCAAGTCAGAGTATCATAGTCAGATTCCAAAGAGCT 325
Qy 222 GAAGATCTATCTCTTGTATATGTTGCTGAGCAGCAATATCAACAGAGGGGCCAACAGA 281
Db 326 GAAGATCTATCTCTTGTATATGTTGCTGAGCAGCAATATCAACAGAGGGGCCAACAGA 385
Qy 282 AAGCAGAGGAGGAGCTCAAGAGCTGGAAGAGATGTTTGAAGAAAGAGCTGAAGAAAGGTG 341
Db 386 AAGCAGAGGAGGAGCTCAAGAGCTGGAAGAGATGTTTGAAGAAAGAGCTGAAGAAAGGTG 445
Qy 342 TTCCCTCAATTTGTATATGATGATGAGAGATGACAGATGAAGCCCTCAGATCCAG 401
Db 446 TTCCCTCAATTTGTATATGATGATGAGAGATGACAGATGAAGCCCTCAGATCCAG 505
Qy 402 AATCTGTACAAAGATGATCTTGTATCAAAACCCGGAATATCTTTGCTGAGATGCATGT 461
Db 506 AATCTGTACAAAGATGATCTTGTATCAAAACCCGGAATATCTTTGCTGAGATGCATGT 565
Qy 462 GGCAGACAGCATTTACAGATTTAGATGATGCTGTAATGGGTCTGCAATGCAATCTTA 521
Db 566 GGCAGACAGCATTTACAGATTTAGATGATGCTGTAATGGGTCTGCAATGCAATCTTA 625
Qy 522 TTACTGATCGAAAACTTTTAAAGATACCTTGTGTAATTTCCAGTTCTATACGTCCTTA 581
Db 626 TTACTGATCGAAAACTTTTAAAGATACCTTGTGTAATTTCCAGTTCTATACGTCCTTA 685
Qy 582 ATGAATCTCGTTTAAAGAGCAGCATTAATACAACTGTATTATCCATGGGGCCCTGAAC 641
Db 686 ATGAATCTCGTTTAAAGAGCAGCATTAATACAACTGTATTATCCATGGGGCCCTGAAC 745
Qy 642 AATCCCTCTTCCCGAAGAAAGACT-CCCTTGGCCCTCCAAACCATCAATG-CTTTAGAG 699
Db 746 AATCCCTCTTCCCGAAGAAAGACT-CCCTTGGCCCTCCAAACCATCAATG-CTTTAGAG 805
Qy 700 AAGAAAGTCGT-GGATTTCTTACACAGTGAAGAAATTTTCAGAGTCTGTATTAAG 758
Db 806 AAGAAAGTCGTGGATTTCTTACACAGTGAAGAAATTTTTTTCAGAGTCTGTATTAAG 865
Qy 759 ACACAACTTA 771
Db 866 AAGACACACNACNA 878

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RESULT 10

CA441688/c
LOCUS CA441688 635 bp mRNA linear EST 08-NOV-2002
DEFINITION UI-H-ED0-ax1-a-05-0-UI.s1 NCI CGAP ED0 Homo sapiens CDNA clone
UI-H-ED0-ax1-a-05-0-UI 3', mRNA sequence.
ACCESSION CA441688
VERSION CA441688.1 GI:24806108
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 635)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA library preparation: Dr. M. Bento Soares, University of Iowa
CDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this CDNA
sequence: 1-54, >AT rich#low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
source

Location/Qualifiers
1..635
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-ED0-ax1-a-05-0-UI"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_1ib="NCI CGAP ED0"
/note="Organ: Left Pubic Bone; Vector: pT73-Pac
(pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI CGAP ED0 is a CDNA library containing
the following tissue(s): Chondrosarcoma cell line C55. The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
CDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT73-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is GCTCAAGCT.
TAG_TISSUE=chondrosarcoma
TAG_Lib=UI-H-ED0
TAG_SEQ=CTCAAGCT"

ORIGIN

Query Match 22.5%; Score 610; DB 6; Length 635;
Best Local Similarity 100.0%; Pred. No. 3.1e-131;
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2108 CAAGCAAAAAGTTGATTCGATTAAGTATATGTTGCAAGAGCTTTATATTA 2167
Db 635 CAAGCAAAAAGTTGATTCGATTAAGTATATGTTGCAAGAGCTTTATATTA 576
Qy 2168 TGGTATTAATGAAGATATTTTGTATATGACAGATATTTATATATGCTGTC 2227
Db 575 TGGTATTAATGAAGATATTTTGTATATGACAGATATTTATATATGCTGTC 516
Qy 2228 ATTACACTTAAGTCACAGAAAAAATATATCATGCTTACTCAGGCTTTCTTAAAAATTA 2287
Db 515 ATTACACTTAAGTCACAGAAAAAATATATCATGCTTACTCAGGCTTTCTTAAAAATTA 456

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QY 2288 ATTTTATAGAGATCTTGAAGTAAAGACATTTTCTTAATTTCTTTTCTTATTCCTCA 2347
 DB 455 ATTTTATAGAGATCTTGAAGTAAAGACATTTTCTTAATTTCTTTTCTTATTCCTCA 396
 QY 2348 CTTGTATATCCCTTACAGATCCGGATTCGACACATCTTTTGGAGTTACCTCTTCA 2407
 DB 395 CTTGTATATCCCTTACAGATCCGGATTCGACACATCTTTTGGAGTTACCTCTTCA 336
 QY 2408 AGCCATGAACCAAAAGTTCTATAGAGATCAAGTAAAGTCAAGCTCTTATTCGT 2467
 DB 335 AGCCATGAACCAAAAGTTCTATAGAGATCAAGTAAAGTCAAGCTCTTATTCGT 276
 QY 2468 AGTACTTATTAAGAGAGAGATGTTTCTATTCAGTAAAGTCAATTTTCTTACGCTTAAG 2527
 DB 275 AGTACTTATTAAGAGAGATGTTTCTATTCAGTAAAGTCAATTTTCTTACGCTTAAG 216
 QY 2528 TTCTGATAGAGATCTTGAAGTAAAGTCAATTTTCTTATTCAGTAAAGTCAATTTT 2587
 DB 215 TTCTGATAGAGATCTTGAAGTAAAGTCAATTTTCTTATTCAGTAAAGTCAATTTT 156
 QY 2588 TTTCGATATGCTTCTTGAAGTAAAGTCAATTTTCTTATTCAGTAAAGTCAATTTT 2647
 DB 155 TTTCGATATGCTTCTTGAAGTAAAGTCAATTTTCTTATTCAGTAAAGTCAATTTT 96
 QY 2648 TTTTCATGCTTCTTGAAGTAAAGTCAATTTTCTTATTCAGTAAAGTCAATTTT 2707
 DB 95 TTTTCATGCTTCTTGAAGTAAAGTCAATTTTCTTATTCAGTAAAGTCAATTTT 36
 QY 2708 TTTTATCTTT 2717
 DB 35 TTTTATCTTT 26

RESULT 11
 BI493312 615 bp mRNA 1linear EST 28-AUG-2001
 LOCUS df99g06.y1 Morton Fetal Cochlea Homo sapiens cDNA clone
 DEFINITION IMAGE:2540746 5', mRNA sequence.
 BI493312
 VERSION BI493312.1 GI:15332656
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 615)
 Roberton, N.G., Khetarpal, U., Gutierrez-Espeleta, G.A., Bleher, F.R. and Morton, C.C. Isolation of novel and known genes from a human fetal cochlear cDNA library using subtractive hybridization and differential screening Genomics 23, 42-50 (1994)
 95130111
 7829101
 Contact: Morton, C. C.
 Departments of Pathology and Obstetrics, Gynecology and Reproductive Biology
 Brigham and Women's Hospital
 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
 Tel: 617 732 7980
 Fax: 617 732 6996
 Email: cmorton@rics.bwh.harvard.edu
 DNA sequencing and analyses were performed by National Institutes of Health Intramural Sequencing Center (NISC; see http://www.nisc.nih.gov).
 This clone is available royalty-free through LBNL; contact the IMAG Consortium (info@image.llnl.gov) for further information.
 Plate: LBNL6328 Row: N Column: 11
 Seq primer: M13RP1 reverse primer (ABI).
 Location/Qualifiers
 1. 615
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"

ORIGIN
 Query Match 22.3%; Score 606.4; DB 4; Length 615;
 Best Local Similarity 99.8%; Pred. No. 2.2e-130;
 Matches 607; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

/clone="IMAGE:2540746"
 /csize_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_1lb="Morton Fetal Cochlea"
 /note="Organ: ear; Vector: pBluescript SK-; Site: 1: EcoRI; Site: 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned unidirectionally. Primer: 0150 dt. Fetal cochlea, normal. 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP XR Vector. Library constructed by N. Roberton, C. Morton. -5' adaptor sequence: 5' GAATTCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3' "

QY 2038 CAAAAGGGAACAGCAAAAAGTTGATTCGATTAAGTATGTAATGTCAGAAAG 2157
 DB 8 CAAAAGGGAACAGCAAAAAGTTGATTCGATTAAGTATGTAATGTCAGAAAG 67
 QY 2158 GCTTATATATGCTTATATGAAGATTTTGTATATGACGATTAATTTA 2217
 DB 68 GCTTATATATGCTTATATGAAGATTTTGTATATGACGATTAATTTA 127
 QY 2218 TATATGCTGATTAACATTAAGTCAAGGAAAAATATATGCTTACTAGGCTTC 2277
 DB 128 TATATGCTGATTAACATTAAGTCAAGGAAAAATATATGCTTACTAGGCTTC 187
 QY 2278 TTAATAATTAATTTTATATGAGATCTTGAAGTAAAGACATTTTCTTTTTC 2337
 DB 188 TTAATAATTAATTTTATATGAGATCTTGAAGTAAAGACATTTTCTTTTTC 247
 QY 2338 TTAATCCCACTGATATATCCCTTACAGTACCGGATCTGACATCTTTTGAGAT 2397
 DB 248 TTAATCCCACTGATATATCCCTTACAGTACCGGATCTGACATCTTTTGAGAT 307
 QY 2398 ACCCTCTATGAGCATGACCAAAAAGTTCTATGAGAGATCAAGTAAAGTCAAGCTTC 2457
 DB 308 ACCCTCTATGAGCATGACCAAAAAGTTCTATGAGAGATCAAGTAAAGTCAAGCTTC 367
 QY 2458 CTATTCGTGATGACTTATTAAGAGAGATGTTTCTATTCATTCATTCATTCATTC 2517
 DB 368 CTATTCGTGATGACTTATTAAGAGAGATGTTTCTATTCATTCATTCATTCATTC 427
 QY 2518 AGCCTTAAGTCTGATATGAGTCTTACTACCTCTCTTTTCTAGTTTCATATATAG 2577
 DB 428 AGCCTTAAGTCTGATATGAGTCTTACTACCTCTCTTTTCTAGTTTCATATATAG 487
 QY 2578 TATTCATTTTGGCATATAGCTTCTGTAAGCAATTTATATATCTATTAATTAACATG 2637
 DB 488 TATTCATTTTGGCATATAGCTTCTGTAAGCAATTTATATATCTATTAATTAACATG 547
 QY 2638 AACTGCCACCTCTTATGCTTCCCAAACTTGGGGCAATTTGATGCTATTTTAA 2697
 DB 548 AACTGCCACCTCTTATGCTTCCCAAACTTGGGGCAATTTGATGCTATTTTAA 607
 QY 2698 AATAAATG 2705
 DB 608 AATAAATG 615

RESULT 12
 BI493311/c 613 bp mRNA 1linear EST 28-AUG-2001
 LOCUS df99g06.w1 Morton Fetal Cochlea Homo sapiens cDNA clone
 DEFINITION IMAGE:2540746 3', mRNA sequence.
 BI493311
 VERSION BI493311.1 GI:15332655
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE AUTHORS	TITLE	JOURNAL MEDLINE PUBMED	COMMENT
1 (bases 1 to 613)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
Robertson,N.G., Khetarpal,U., Gutierrez-Espeleta,G.A., Bieber,F.R. and Morton,C.C.	Isolation of novel and known genes from a human fetal cochlear cDNA library using subtractive hybridization and a human fetal cochlear screening	Genomics 23, 42-50 (1994)	
		9513011	
		7829101	
	Contact: Morton, C. C. Departments of Pathology and Obstetrics, Gynecology and Reproductive Biology Brigham and Women's Hospital 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA Tel: 617 732 7980 Fax: 617 738 6996 Email: cmorton@rics.bwh.harvard.edu DNA sequencing and analyses were performed by National Institutes of Health Intramural Sequencing Center (NISC; see http://www.nisc.nih.gov). This clone is available royalty-free through LBNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Plate: LLM6528 Row: N Column: 11 Seq primer: 17 primer.		
FEATURES	Location/Qualifiers		
source	1..613 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:2540746" /tissue_type="cochlea" /dev_stage="16-22 week fetus" /lab_host="SOLR cells (kanamycin resistant)" /clone_lib="Morton Fetal Cochlea" /note="Organ: ear; Vector: pBluescript SK-; Site 1: EcoRI, Site 2: XhoI; Reference: Genomics 23, 42-50 (1994) cloned unidirectionally. Primer: Oligo dt. Fetal cochlea, normal, 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP XR Vector. Library constructed by N. Robertson, C. Morton. -5' adaptor sequence: 5' GAATTCGACGACG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'."		
ORIGIN			
Query Match	22.2%;	Score 602.8;	DB 4; Length 613;
Best Local Similarity	99.7%;	Pred. No. 1.5e-129;	
Matches 604;	Conservative 0;	Mismatches 2;	Indels 0; Gaps 0;
QY	2098 CAAAGGGAACAAGCAAAAAGTTGGATTCGATTAAGTATCTATTAGTCAGAG	2157	
DB	606 CAAAAGGGAACAAGCAAAAAGTTGGATTCGATTAAGTATCTATTAGTCAGAG	547	
QY	2158 GCTTATATATGCTATATATGAAAAAGATTTTTTGTATATTTGATATTTGA	2217	
DB	546 GCTTATATATGCTATATATGAAAAAGATTTTTTGTATATTTGATATTTGA	487	
QY	2218 TAAATGCTGTCATTACACTTAAAGTACACGAAAAAATATACATGCTTACT	2277	
DB	486 TAAATGCTGTCATTACACTTAAAGTACACGAAAAAATATACATGCTTACT	427	
QY	2278 TTAATAAATAAATTTTTTATAGAGATCCTTGAGTAAAGACATTTTGGTAA	2337	
DB	426 TTAATAAATAAATTTTTTATAGAGATCCTTGAGTAAAGACATTTTGGTAA	367	
QY	2338 TTATTCGCCACTTGTATATCCCTTACAGATACGGGATCTGCACACATCT	2397	
DB	366 TTATTCGCCACTTGTATATCCCTTACAGATACGGGATCTGCACACATCT	307	
QY	2398 ACGCTTCATATGCGCATGACCAAAAGCTTCTATGAGAGCATGCAAGTAAG	2457	
DB	306 ACGCTTCATATGCGCATGACCAAAAGCTTCTATGAGAGCATGCAAGTAAG	247	
QY	2458 CTATTCGTGTAGTACTTATTAAGAGAGAGATGTTTTTCATTCGATTAAG	2517	

Db	246	CTATTCGTAGACACTTATTAGAGAGAAATGGTTTCAATTCATGATGACATTTTCTT	187
Oy	2518	AGCCTTAACGTTCTGATATAGACTTACTACTCACTTCTCTTTTTCAGTTTTCATAATPAAG	2577
Db	186	AGCCTTAACGTTCTGATATAGACTTACTACTCACTTCTCTTTTTCAGTTTTCATAATPAAG	127
Oy	2578	TATTCATTTTTTGGCCATTAATGCTGCTGCTGAAAGCCAAATTTTATATCTAATATAAATG	2637
Db	126	TATTCATTTTTTGGCCATTAATGCTGCTGCTGAAAGCCAAATTTTATATCTAATATAAATG	67
Oy	2638	AACGCCACACTCTTCATGACCTGCGCAAATTGCGGCAATTGATGCTAATAAGTATTTTAA	2697
Db	66	AACGCCACACTCTTCATGACCTGCGCAAATTGCGGCAATTGATGATATAATGATATTTTAA	7
Oy	2698	AATATAA	2703
Db	6	AATATAA	1
RESULT 13			
LOCUS	CD638761	585 bp	mRNA
DEFINITION	AGENCOURT_14535036 NIH_MGC_191 Homo sapiens CDNA clone	linear	EST 17-JUN-2003
ACCESSION	CD638761		
VERSION	IMAGE:30417403 5', mRNA sequence.		
KEYWORDS	CD638761.1 GI:31804901		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 585)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Daniela S. Gerhard, Ph.D.		
	Office of Cancer Genomics		
	National Cancer Institute / NIH		
	Bldg. 31 Rm10A07 Bethesda, MD 20892		
	Email: cgabs-remail.nih.gov		
	Tissue Procurement: Narayan Bhat		
	CDNA Library Preparation: CLONTECH Laboratories, Inc.		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNase Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.lnl.gov		
	plate: NDCM218 row: 1 column: 20		
	High quality sequence stop: 548.		
FEATURES	Location/Qualifiers		
source	1..585		
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	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:30417403"		
	/issue_type="Pooled"		
	/lead_host="DH10B (T1 phage-resistant)"		
	/clone_id="NIH_MGC_191"		
	/note="Vector: pDNR-LIB; Site 1: SfiI (ggccatcaggcc);		
	Site 2: SfiI (ggccgcctggcc); Library is oligo-dT primed		
	and directionally cloned. PBMC - Peripheral Blood		
	Mononuclear Cells. RNA was pooled from 3/6hour stimulation		
	with PMA adn Ionomycin. 5' and 3' adaptors were used in		
	cloning as follows: 5' adaptor sequence:		
	5'-CACGCCATTATGCCC-3' and 3' adaptor sequence:		
	5'-ATTCTAGAGCCAGCGCGCCGACATG-dt(30)BN-3' (where B = A,		
	C, or G and N = A, C, G, or T). Average insert size 1.69		
	kb (range 0.70-5.0 kb). 15/15 colonies contained inserts		
	by PCR. This library was enriched for full-length clones		
	and was constructed by Clontech Laboratories (Palo Alto,		
	CA). Note: this is a NIH_MGC Library."		

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 533)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

JOURNAL

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

COMMENT

CDNA library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 487.
Location/Qualifiers
1..533

FEATURES

source

/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:3214345"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu24"
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI CGAP Lu5 was prepared, and as circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (cloneids
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaudo."

ORIGIN

Query Match 19.6%; Score 533; DB 2; Length 533;
Best Local Similarity 100.0%; Pred. No. 2.8e-113;
Matches 533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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533 ATATTTTGTATATGACAGATTAATTTTATGCTGATTAACCTTAAGTCA 474

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|||||
473 CAGAAAAAATATACATGCTTACTCAGGCTTTCTTAAAAATAAATTTTATAGATCC 414

2304 TTGAGTAAAGACATTTGCTTAATTTCTTTTCTTATCCGACCTGTATATCCCTAC 2363
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413 TTGAGTAAAGACATTTGCTTAATTTCTTTTCTTATCCGACCTGTATATCCCTAC 354

2364 CAGTACCGGGATCTGCACATCTTTTGAGTTACCTCTTCATAGCAGCAACCAAC 2423
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353 CAGTACCGGGATCTGCACATCTTTTGAGTTACCTCTTCATAGCAGCAACCAAC 294

2424 GTTCTATGAGAGATGAGTAAGTCAAGCTCTTATCTGTAGTACTTATAGAGA 2483
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293 GTTCTATGAGAGATGAGTAAGTCAAGCTCTTATCTGTAGTACTTATAGAGA 234

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2544 CTACTCACTTCCTTTTTCAGTTTTCATATAGTATTCATTTTTCGCAATATGCTTC 2603
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173 CTACTCACTTCCTTTTTCAGTTTTCATATAGTATTCATTTTTCGCAATATGCTTC 114

QY 2604 CTGTAAGCCAAATTTTATATCTAATTAACATGAACTGCCACTTTCATGCTGCCAA 2663
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QY 2664 ACTTGGGCAATGTATGCTAAATGCTATTTTAAATATATGTTTATTCCT 2716
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DB 53 ACTTGGGCAATGTATGCTAAATGCTATTTTAAATATATGTTTATTCCT 1

Search completed: September 23, 2005, 08:29:10
Job time : 8591 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 22, 2005, 23:40:50; Search time 1408 Seconds

(without alignments)
11423.251 Million cell updates/sec

Title: US-10-617-217a-88

Perfect score: 2717
Sequence: 1 aaaggaagacagaaagcc.....aataatgctttattcttc 2717

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: N_Geneseq_16Dec04:*

1: geneeqn19808:*\n2: geneeqn19908:*\n3: geneeqn20005:*\n4: geneeqn2001as:*\n5: geneeqn2001bs:*\n6: geneeqn2002as:*\n7: geneeqn2002bs:*\n8: geneeqn2003as:*\n9: geneeqn2003bs:*\n10: geneeqn2003cs:*\n11: geneeqn2003ds:*\n12: geneeqn2004as:*\n13: geneeqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2717	100.0	2717	6	AB091955 Human NF-
2	1835.8	67.6	1860	4	AA776847 Human sec
3	1337.4	49.2	2171	10	AD030553 Human nov
4	880.6	32.4	1687	4	AAK94557 Human ful
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6	476.2	17.5	533	4	AAK93015 Human CDN
7	476.2	17.5	533	12	ADL29442 3' end of
8	469.4	17.3	522	10	AD032380 Human nov
9	243	8.9	253	6	ABN96310 Gene #280
10	156.4	3.8	660	10	ACD94489 Human col
11	103.6	3.8	104	2	AAK10464 Human b1a
12	58.4	2.1	8995	6	ABN46564 Human bpl
13	58.4	2.1	8995	6	ABN32333 Human imm
14	50.8	1.9	5378	6	ABJ33879 Human imm
15	50.8	1.9	10543	6	ABK31249 Signal tr
16	50.8	1.9	10543	6	ABL70206 Chemical1
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18	50	1.8	2000	8	ADA71938 Rice gene
19	50	1.8	5586	6	ABK40003 Human che
20	50	1.8	50000	6	ABJ56202 AmePV gen

ALIGNMENTS

21	49.8	1.8	6876	6	ABJ32981 Human imm
22	49.8	1.8	17131	6	ABJ33053 Human imm
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24	49.4	1.8	11422	6	ABJ32219 Human imm
25	49	1.8	6127	6	ABJ34448 Human met
26	49	1.8	6127	6	ABJ70119 Human met
27	49	1.8	6127	7	ADS99709 Human imm
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RESULT 1	AB091955	standard; cDNA; 2717 BP.
ID	AB091955	standard; cDNA; 2717 BP.
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AC	30-SEP-2002	(first entry)
DT	Human NF-kB activating gene SEQ ID NO 88.	
DE	Human NF-kB activating gene SEQ ID NO 88.	
XX	Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;	
KW	immunomodulator; cytosolic; antiinfective; osteopathic; noctropic;	
KW	neuroprotective; anti-HIV; autoimmune disease; cancer; infection;	
KW	bone disease; AIDS; neurodegenerative disease; ischaemic disorder; gene;	
KW	ss.	
OS	Homo sapiens.	
XX	WO200253737-A1.	
FN	11-JUL-2002.	
XX	25-DEC-2001; 2001WO-JP011389.	
PD	28-DEC-2000; 2000JP-00402288.	
XX	26-MAR-2001; 2001JP-00088912.	
PR	24-AUG-2001; 2001JP-00254018.	
XX	(ASAH) ASAH KASEI KOGYO KK.	
PA	Mateuda A, Honda G, Muramatsu S, Nagano Y;	
PI	WPI, 2002-583617/62.	
XX	P-PSDB; ABP61467.	
DR	NF-approximately KB activating gene and expressed protein, applicable in	
XX	diagnosis and screening inhibitors or promoters to control excessive	
PT	activation or inhibition for treating e.g. inflammations, autoimmune	
PT	diseases and cancer.	
XX	Claim 4; Page 403-407; 84pp; Japanese.	
PS	The invention relates to a purified protein (I), comprising one of 90	
XX		
CC		

CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of
CC the sequences but with some amino acids deleted, substituted or added and
CC with a NF- κ B (nuclear factor kappa B) activating effect. The protein and
CC encoding gene (AB091912-AB092001) are useful in diagnosis and screening
CC inhibitors or promoters to control excessive activation or inhibition and
CC for treating e.g. inflammations, autoimmune diseases, cancers,
CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic
CC disorders
XX

Sequence 2717 BP; 840 A; 504 C; 541 G; 832 T; 0 U; 0 Other;

Query Match 100.0%; Score 2717; DB 6; Length 2717;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 RESULT 2
 ID AAF76847 standard; cDNA; 1860 BP.
 XX AAF76847;
 AC AAF76847;
 DT 14-MAY-2001 (first entry)
 DE Human secreted protein cDNA #5.
 DE Human; secreted protein; immunomodulatory; antileukemic; dermatological;
 KM immunosuppressive; anti-inflammatory; anti-HIV; immunostimulant;
 KM cytotoxic; cardiant; vascular; anti-angiogenic; ophthalmological;
 KM neuroprotectant; neurotropic; anticonvulsant; vaccine; antialzheimer's;
 KM antiparkinsonian; antimicrobial; vulnary; gene therapy;
 KM immune disorder; hyperproliferative; cardiovascular; angiogenic;
 KM neurological; infection; ss.
 XX Homo sapiens.
 OS

XX PN WO200112776-A2.
 XX PD 22-FEB-2001.
 XX PF 15-AUG-2000; 2000WO-US022350.
 XX PR 16-AUG-1999; 99US-0148759P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Shi Y, Young PE, Ebner R, Soppet DR, Ruden SM;
 DR WPI; 2001-244245/25.
 DR P-PSDB; AAB70066.
 PT Nucleic acids encoding 18 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease
 PT and diabetic retinopathy.
 PS Claim 1; Page 350-351; 380pp; English.
 CC The present sequence is one of 18 nucleic acid molecules encoding novel
 CC human secreted proteins. The nucleic acids and proteins may be used in
 CC the prevention, diagnosis and treatment of diseases including immune
 CC disorders (e.g. multiple sclerosis, systemic lupus erythematosus and
 CC human immunodeficiency virus (HIV) infections), hyperproliferative
 CC disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases
 CC (e.g. Scimitar syndrome, Chaga's cardiomyopathy and coronary
 CC arteriosclerosis), angiogenic disorders (e.g. corneal graft
 CC neovascularisation and diabetic retinopathy), neurological disorders
 CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease),
 CC infectious diseases and/or for promoting wound healing, regeneration
 CC and/or chemoraxis. The nucleic acid molecules may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar nucleic acid sequences in samples. The polypeptides may also be
 CC used as antigens in the production of antibodies and in assays to
 CC identify modulators of protein expression and activity
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 Query Match 67.6%; Score 1835.8; DB 4; Length 1860;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1837; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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 QY 405 CTGCTACAAAGATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 464
 DB 82 CTGCTACAAAGATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 141
 QY 465 AGACAGCATTTTACAGAAATTTAGATGATGATGATGATGATGATGATGATGATGAT 524
 DB 142 AGACAGCATTTTACAGAAATTTAGATGATGATGATGATGATGATGATGATGATGAT 201
 QY 525 CTGACTGAAAATCTTTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 584
 DB 202 CTGACTGAAAATCTTTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 261
 QY 585 AACTCCGTTTAAAGGAGCATTAATACAACTCTGTTATACCATGCGGCGCTGAACAT 644
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 DB 562 AGCAGTTTCTAGAAATGTTTAAATPAAAGAGCTTCACTTAAAGAAACCTATGAG 621
 QY 945 CACAAGAAAGATTAATTTCTGACAGACAGCTATAAAATTTGATGATCTTTGATGTTTC 1004
 DB 622 CACAAGAAAGATTAATTTCTGACAGACAGCTATAAAATTTGATGATCTTTGATGTTTC 681
 QY 1005 AGTAAACTTGACATTTGTCAGAGTTTCAAGACCTTTCTTCAAAATTTTCTAGTTCAATG 1064
 DB 682 AGTAAACTTGACATTTGTCAGAGTTTCAAGACCTTTCTTCAAAATTTTCTAGTTCAATG 741
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 DB 1042 TTTTAAAAAGAAACCAAGTCAATGATTTTCTGCTGAAATCTGCATATTTGAGGCACTT 1101
 QY 1425 CCCACACCGATTCACGCCCATTTGATGATGAGTGAAGTGAAGGACTTGTGAGAGGTG 1484
 DB 1102 CCCACACCGATTCACGCCCATTTGATGATGAGTGAAGTGAAGGACTTGTGAGAGGTG 1161
 QY 1485 TTGACAGCGTCCCTGAGGCTTAAATCTCTCAATATTAGTCATCATTTGTAATGAGCTT 1544
 DB 1162 TTGACAGCGTCCCTGAGGCTTAAATCTCTCAATATTAGTCATCATTTGTAATGAGCTT 1221
 QY 1545 TATTTCGACAGCTTCTAAAAAGCGTATACTGTGAGAGGCGCAATATTCCTTTTAA 1604
 DB 1222 TATTTCGACAGCTTCTAAAAAGCGTATACTGTGAGAGGCGCAATATTCCTTTTAA 1281
 QY 1605 ATCAAAAAACCTCTCTTATGAAAGCTTTAAAGCTTCCGTCACACAAATTTCTCTGAG 1664
 DB 1282 ATCAAAAAACCTCTCTTATGAAAGCTTTAAAGCTTCCGTCACACAAATTTCTCTGAG 1341
 QY 1665 GAAAGTATTTCTCAATTAGGCTTCAAAAGTACCTGACTGCTGTCATGTCGTGTGATTA 1724
 DB 1342 GAAAGTATTTCTCAATTAGGCTTCAAAAGTACCTGACTGCTGTCATGTCGTGTGATTA 1401
 QY 1725 GGTATATTTATAAGACTTTGATAGAGAGATTTTATTAATCTCTATTTCTAGAGC 1784
 DB 1402 GGTATATTTATAAGACTTTGATAGAGAGATTTTATTAATCTCTATTTCTAGAGC 1461
 QY 1785 CCCATGCTCTTAACAAGCAGAGAGGCCCAAAACAGATTTGTTCTTCTCCACAGGCC 1844
 DB 1462 CCCATGCTCTTAACAAGCAGAGAGGCCCAAAACAGATTTGTTCTTCTCCACAGGCC 1521
 QY 1845 TTCTGCCCATCTGAGATTGAGGAGAGCATGTCACCTTGAGATCAGGAGTGGGGTGAAGA 1904

DB 1522 TTCTGCCCATCTGAGATTGAGGAGAGCATGTCACCTTAGATCAGAGATGGGGTGAAGA 1581
 QY 1905 TGGGTCATGTCATGTAATGAGAAAAAGCCCTCTTGGGATCATGAGACTTTGGTTCTAGTCC 1964
 DB 1582 TGGGTCATGTCATGTAATGAGAAAAAGCCCTCTTGGGATCATGAGACTTTGGTTCTAGTCC 1641
 QY 1965 AATTTCTGCACTGAGATGTAATGTAATCTGTGGGCAACTATTTACCTCTTATCTGT 2024
 DB 1642 AATTTCTGCACTGAGATGTAATGTAATCTGTGGGCAACTATTTACCTCTTATCTGT 1701
 QY 2025 GAAATGAAAGGCTTGAATGTAATGTAATCTTAAAGCTTTGTCTCTATGAGATGTA 2084
 DB 1702 GAAATGAAAGGCTTGAATGTAATGTAATCTTAAAGCTTTGTCTCTATGAGATGTA 1761
 QY 2085 AAACCTAGGACCAAAAAGGGAACAAGCAAAAAAGTTTGATTCGATTAAGTGAATGTA 2144
 DB 1762 AAACCTAGGACCAAAAAGGGAACAAGCAAAAAAGTTTGATTCGATTAAGTGAATGTA 1821
 QY 2145 ATAGTTCAGAAAGCTTATATATGCTTATATGTAATGTAAG 2183
 DB 1822 ATAGTTCAGAAAGCTTATATATGCTTATATGTAATGTAAG 1860
 RESULT 3
 ADC30553 ID ADC30553 standard; cDNA: 2171 BP.
 XX
 AC ADC30553;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human novel cDNA sequence, SEQ ID NO:635.
 XX
 KM Human; diagnostic; drug screening; forensics; gene mapping;
 KM biodiversity assessment; Parkinson's disease; Alzheimer's disease;
 KM neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
 KM ulcers; osteoporosis; autoimmune disease; cancer;
 KM molecular weight marker; food supplement; antiparkinsonian; nootropic;
 KM neuroprotective; anti-inflammatory; anticoagulant; thrombolytic; vulnary;
 KM anticancer; osteopathic; immunosuppressive; anti-inflammatory; cytostatic;
 KM gene therapy; chromosome 5; gene; 88.
 OS Homo sapiens.
 XX
 PN MO2003029271-A2.
 PD 10-APR-2003.
 XX
 PF 24-SEP-2002; 2002WO-US030474.
 XX
 PR 24-SEP-2001; 2001US-0324631P.
 XX
 PA (HISE-) HXSEQ INC.
 XX
 PI Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T,
 PI Zhou P, Ghost M, Wang D, Ma Y, Aundi V, Wang Z, Wang G,
 PI Haley-Vicente D, Drmanac RT;
 XX
 DR WPI: 2003-371981/35.
 DR P-PSDB; ADC31524.
 XX
 PT New polynucleotide and polypeptide useful for diagnosing, preventing or
 PT treating conditions such as neurodegenerative diseases, anemias, platelet
 PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
 PT cancer.
 PT
 PS Claim 1; SEQ ID NO 635; 1185bp; English.
 CC The invention relates to 971 novel human cDNA sequences (ADC29919-
 CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
 CC invention also relates to nucleic acid sequences over 99% identical with
 CC the novel human cDNAs. The invention additionally encompasses expression

CC vectors and host cells comprising a nucleic acid of the invention; the
CC recombinant production of a polypeptide of the invention; an antibody
CC against a polypeptide of the invention; a method of detecting
CC polynucleotides or polypeptides of the invention; and method of
CC identifying a compound which binds to a polypeptide of the invention. The
CC invention further discloses methods of preventing, treating or
CC ameliorating a medical condition; kits comprising polynucleotide probes
CC and/or monoclonal antibodies for carrying out the methods of the
CC invention; methods for the identification of compounds that modulate the
CC expression or activity of the polynucleotide and/or polypeptide; and 767
CC coding sequences corresponding to the cDNA sequences of the invention
CC (ADC31661-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC -ADC33394). The nucleic acids and polypeptides of the invention are
CC useful in diagnostics, drug screening, forensics, gene mapping, in the
CC identification of mutations responsible for genetic disorders or other
CC traits, for assessing biodiversity, and in producing many other types of
CC data and products dependent on DNA and amino acid sequences. They are
CC also used for treating diseases such as Parkinson's disease, Alzheimer's
CC disease and other neurodegenerative diseases, anaemia, platelet
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers
CC and as food supplements. The present sequence represents a specifically
CC claimed human cDNA sequence of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPRO at
CC ftp.wipro.int/pub/published_pcr_sequences.

XX Sequence 2171 BP; 673 A; 448 C; 468 G; 582 T; 0 U; 0 Other;

Query Match 49.2%; Score 1337.4; DB 10; Length 2171;
Best Local Similarity 98.8%; Pred. NO. 0;
Matches 1347; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 70 GAATACATTAAGTTTCTCTCTGCTGGATTTTATTAATGGGTATCGGAAGTCTA 129
Db 414 GAAATACATTAAGTTTCTCTCTGCTGGATTTTATTAATGGGTATCGGAAGTCTA 473
QY 130 AATTAATTCCTGCGCTCTCTCTGCTGGATTTTATTAATGGGTATCGGAAGTCTA 189
Db 474 AATTAATTCCTGCGCTCTCTCTGCTGGATTTTATTAATGGGTATCGGAAGTCTA 533
QY 190 CAGATATCATGATGATGATTCAGAAAGTCTGATCTATCTTGTATATGTTGCTG 249
Db 534 CAGATATCATGATGATGATTCAGAAAGTCTGATCTATCTTGTATATGTTGCTG 593
QY 250 AGCAGCATATCAACAGAGGGCCCAACAGAAAGCAGAGGAGCTCAAGCGTGAAG 309
Db 594 AGCAGCATATCAACAGAGGGCCCAACAGAAAGCAGAGGAGCTCAAGCGTGAAG 653
QY 310 AGATGTTGAAGAAGAACTGAAAGAGGTTCTCAAAATTTGTGATTTGATGAG 369
Db 654 AGATGTTGAAGAAGAACTGAAAGAGGTTCTCAAAATTTGTGATTTGATGAG 713
QY 370 AAGATGACAGATGAAGCCCTCAGAGTCCAGAACTCTCTACAGATGATCTTGTATCA 429
Db 714 AAGATGACAGATGAAGCCCTCAGAGTCCAGAACTCTCTACAGATGATCTTGTATCA 773
QY 430 AACCAGGAATATCTTTCTGATGATGCAATGTGGCAGACAGATTTACAGAAATTTAGTG 489
Db 774 AACCAGGAATATCTTTCTGATGATGCAATGTGGCAGACAGATTTACAGAAATTTAGTG 833
QY 490 ATGCTGTAATGGGTCTGATGAGCAATCTTATTTCTAGCTGAAGAACTTTTAAAGATA 549
Db 834 ATGCTGTAATGGGTCTGATGAGCAATCTTATTTCTAGCTGAAGAACTTTTAAAGATA 893
QY 550 CTGGTGTATTTTCCAGTTCTATATAGCTCCCTAATGAATCCGTTAAGCAGCATTAAT 609
Db 894 CTGGTGTATTTTCCAGTTCTATATAGCTCCCTAATGAATCCGTTAAGCAGCATTAAT 953
QY 610 ACAACTCTGTTATACCATGCGGCCCTGAGACAAATCCCTTCCCGAAGAAAGATCCCT 669

Db 954 ACAACTCTGTTATACCATGCGGCCCTGAGACAAATCCCTTCCCGAAGAAAGATCCCT 1013
QY 670 TTGCTCTCAAAACCATCAATGCTCTTAAGAGAAAGATGCTGATTTCTCTACAGAAATG 729
Db 1014 TTGCTCTCAAAACCATCAATGCTCTTAAGAGAAAGATGCTGATTTCTCTACAGAAATG 1073
QY 730 AAGAAATTTTTCAGAGATCTGTGTATTAAGACAAACAATTTATTTGAAAGACAAAGAA 789
Db 1074 AAGAAATTTTTCAGAGATCTGTGTATTAAGACAAACAATTTATTTGAAAGACAAAGAA 1133
QY 790 ATATGTACAAAGCAATTTATGCTGAGATGAATATTAATGATGAGGCTGCTGTG 849
Db 1134 ATATGTACAAAGCAATTTATGCTGAGATGAATATTAATGATGAGGCTGCTGTG 1193
QY 850 TTTTGTAAACCAATGATTAATCTTCACTTGAAGAAAGATTTCTAAGAAATGTTTAAT 909
Db 1194 TTTTGTAAACCAATGATTAATCTTCACTTGAAGAAAGATTTCTAAGAAATGTTTAAT 1253
QY 910 AAGAGAGCTTTCACCTTAAGAAACCTATGAGCAGACAGAAAGATTAATTTCTGACAG 969
Db 1254 AAGAGAGCTTTCACCTTAAGAAACCTATGAGCAGACAGAAAGATTAATTTCTGACAG 1313
QY 970 AAGCTTATTAATTTGTGATCTTTTGAATGTTTCACTTAATCTGACATGTCAGAGTT 1029
Db 1314 AAGCTTATTAATTTGTGATCTTTTGAATGTTTCACTTAATCTGACATGTCAGAGTT 1373
QY 1030 CAGAGCTTTTCTTCACAATTTTCTAATGATGATGATGATGATGATGATGATGATGATG 1089
Db 1374 CAGAGCTTTTCTTCACAATTTTCTAATGATGATGATGATGATGATGATGATGATGATG 1433
QY 1090 ATATTCCTGTATGAACTTGAACAAAACTTGTATGACAGACATTTTAAATGATGAA 1149
Db 1434 ATATTCCTGTATGAACTTGAACAAAACTTGTATGACAGACATTTTAAATGATGAA 1493
QY 1150 CAACATTTATTTCTGAAATTTGATCTCAAGAGACAGAAAGAAATGAGCCACAGA 1209
Db 1494 CAACATTTATTTCTGAAATTTGATCTCAAGAGACAGAAAGAAATGAGCCACAGA 1553
QY 1210 GATCTGATCAACCTTCTCTGAGGACCTCTCATGATGATGATGATGATGATGATGATG 1269
Db 1554 GATCTGATCAACCTTCTCTGAGGACCTCTCATGATGATGATGATGATGATGATGATG 1613
QY 1270 CTATCACCCAGAAATATGAAATGTCAGAAATGAAATTTAGATGATGATGATGATG 1329
Db 1614 CTATCACCCAGAAATATGAAATGTCAGAAATGAAATTTAGATGATGATGATGATGATG 1673
QY 1330 TATTAATTCAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 1389
Db 1674 TATTAATTCAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 1733
QY 1390 ATTTTCTGCTGAATTCGATATTTGAGAGGATTTCCACAC 1432
Db 1734 ATTTTCTGCTGAATTCGAGGCTGCTGATGATGATGATGATGATGATGATGATG 1776

RESULT 4

AAK94557 ID AAK94557 standard; cDNA; 1687 BP.

AAK94557;

06-NOV-2001 (first entry)

Human full-length cDNA, SEQ ID NO: 3459.

Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

Homo sapiens.

EP1130094-A2.

05-SEP-2001.

CC full length human cDNA clone of the invention.

XX Sequence 1687 BP; 458 A; 394 C; 401 G; 434 T; 0 U; 0 Other;

Query Match 32.4%; Score 880.6; DB 12; Length 1687;
Best Local Similarity 99.5%; Pred. No. 76-207;
Matches 883; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

QY 42 TCGCCGATGAGTGAAGAAATGCTGAGAAATATCATTAAGTTTCTCTTCTGCTTGG 101
DB 801 TGGCCATGATGAGAAAGAAATGCTGAGAAATATCATTAAGTTTCTCTTCTGCTTGG 860
QY 102 ATATTATATGAGTATCGGAAAGTCTTAATAATTCCTGCCCTCTTCTCTCTTGG 161
DB 861 ATATTATATGAGTATCGGAAAGTCTTAATAATTCCTGCCCTCTCTCTCTTGG 920
QY 162 GGTAAAGGACAGTGTGATCAAGTCCAGGATATCATGAGTCCAGATCCAAAGTCT 221
DB 921 GGTAAAGGACAGTGTGATCAAGTCCAGGATATCATGAGTCCAGATTCCAAAGTCT 980
QY 222 GAAGATCTATCCTTGTATATGTTGCTGAGCAAGCATATCAACAGAGGGCCAAACAGA 281
DB 981 GAAGATCTATCCTTGTATATGTTGCTGAGCAAGCATATCAACAGAGGGCCAAACAGA 1040
QY 282 AAGCAGAGGAGAGCTCAGAGCGGTGAAAGATGTTTGAAGAAAGAGCTGAAGAGAGTG 341
DB 1041 AAGCAGAGGAGAGCTCAGAGCGGTGAAAGATGTTTGAAGAAAGAGCTGAAGAGAGTG 1100
QY 342 TTCCCTCAATTTGTGATATGATGAGAAATGACACAGATGAAGAGCCCTCAGATCCAG 401
DB 1101 TTCCCTCAATTTGTGATATGATGAGAAATGACACAGATGAAGAGCCCTCAGATCCAG 1160
QY 402 AATCTGCTACAGATGATCTGTATCAACCCGGAAATATCTTGTCTGAGATGCCATG 461
DB 1161 AATCTGCTACAGATGATCTGTATCAACCCGGAAATATCTTGTCTGAGATGCCATG 1220
QY 462 GGCAGACAGCATTTACAGAAATTTAGATGCTGTAATGAGTGTGCTGATGACAAATCTTA 521
DB 1221 GGCAGACAGCATTTACAGAAATTTAGATGCTGTAATGAGTGTGCTGATGACAAATCTTA 1280
QY 522 TTACTGACTGAAAACCTTTTAAGAGATCTGTGTAATTCAGTTCATATCGTCCCTTA 581
DB 1281 TTACTGACTGAAAACCTTTTAAGAGATCTGTGTAATTCAGTTCATATCGTCCCTTA 1340
QY 582 ATGAATCCGCTTAACAGGACGATTAATCAACTCTGTATACCAATGCGGCCCTGAAC 641
DB 1341 ATGAATCCGCTTAACAGGACGATTAATCAACTCTGTATACCAATGCGGCCCTGAAC 1400
QY 642 AATCCCTTCCCGAGAAAGACTCCCTTGGCCCTCCAAACCATCATGCTTTAGAGAA 701
DB 1401 AATCCCTTCCCGAGAAAGACTCCCTTGGCCCTCCAAACCATCATGCTTTAGAGAA 1460
QY 702 GAAAGTCGGATTTCTTACACAGATGAGAAAGATTTTTCAGAGTCGTGTATTAAGCA 761
DB 1461 GAAAGTCGGATTTCTTACACAGATGAGAAAGATTTTTCAGAGTCGTGTATTAAGCA 1520
QY 762 CAACAACATATATGAGAAAGACAAGAAATATGATACAAAGCAATTTATGCTGAGAT 821
DB 1521 CAACAACATATATGAGAAAGACAAGAAATATGATACAAAGCAATTTATGCTGAGAT 1580
QY 822 GAAACATATATCATGTGCTGCTCTTGTGTTGTAACCAAAATGATTAATCTTCACCTGA 881
DB 1581 GAAACATATATCATGTGCTGCTCTTGTGTTGTAACCAAAATGATTAATCTTCACCTGA 1640
QY 882 GAAACATATCTTCTAGAAATGTTTAATAAAGAGATCTTACCTT 928
DB 1641 GAAACATATCTTCTAGAAATGTTTAATAAAGAGATCTTACCTT 1687

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RESULT 6
ID AAK93015/C
AAK93015 standard; cDNA; 533 BP.

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AC AAK93015;
XX 06-NOV-2001 (first entry)
XX Human cDNA 3'-end sequence, SEQ ID NO: 1475.
XX Human, full length cDNA; cDNA synthesis; oligo-capping; ss.
XX Homo sapiens.
XX EP130094-A2.
XX 05-SEP-2001.
XX 07-JUL-2000; 2000BP-00114089.
XX 08-JUL-1999; 99JP-00194486.
XX 11-JAN-2000; 2000JP-0018774.
XX 02-MAY-2000; 2000JP-00183765.
XX (HELI-) HELIX RES INST.
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI, 2001-52425/58.
XX Claim 3, SEQ ID NO 1475; 1380bp + Sequence Listing; English.
XX 830 Primers useful for synthesizing full length cDNA clones and their use
XX in genetic manipulation.
XX
XX The invention relates to primers for synthesizing full length cDNA
XX clones. 830 cDNA molecules encoding a human protein have been isolated
XX and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
XX been determined. Primers for synthesizing the full length cDNA are useful
XX for clarifying the function of the protein encoded by the cDNA. The full
XX length clones were obtained by construction of full length enriched cDNA
XX libraries that were synthesised by the oligo-capping method. The primers
XX enable the production of the full length cDNA easily without any special
XX methods. The present sequence is the nucleotide sequence of the 3'-end of
XX a cDNA provided in the invention. Note: The sequence data for this patent
XX did not form part of the printed specification, but was obtained in CD-
XX ROM format directly from EPO
XX
XX Sequence 533 BP; 150 A; 103 C; 89 G; 175 T; 0 U; 16 Other;
XX
XX Query Match 17.5%; Score 476.2; DB 4; Length 533;
XX Best Local Similarity 93.4%; Pred. No. 3-4e-107;
XX Matches 498; Conservative 0; Mismatches 34; Indels 1; Gaps 1;
QY 396 GTCCAGATCTGCTACAGATGATCTTGTATCAACCCGGAAATATCTTGTCTGAGATG 455
DB 532 GTCCAGATCTTGNANNAAGNGAANTTGTATCAACCCGGATTAATTTTGTATGAGATG 473
QY 456 CCATGTGACAGACAGCATTTACAGAAATTTAGATGCTGTAAATGAGTGTGCTGATGAGCA 515
DB 472 CCATGTGACAGACAGCATTTACAGAAATTTAGATGCTGTAAATGAGTGTGCTGATGAGCA 414
QY 516 ATCTTATATGATGAGTGAAGAACTTTTAAGAGATCTTGTATATTTTCAAGTTCTATAG 575
DB 413 ATCTTATATGATGAGTGAAGAACTTTTAAGAGATCTTGTATATTTTCAAGTTTNAATAG 354
QY 576 TCCCTAATGAATCCGCTTAACAGGACGATTAATCAACTCTGTATACCAATGCGGCC 635
DB 353 TCCCTAATGAATCCGCTTAACAGGACGATTAATCAACTCTGTATACCAATGCGGCC 294
QY 636 CTGAACATATCCCTTCCCGAGAAAGACTCCCTTGGCCCTCCAAACCATCATGCTTGA 695
DB 293 ATGAACATATCCCTTCCCGAGAAAGACTCCCTTGGCCCTCCAAACCATCATGCTTGA 234
QY 696 GAGGAGAAAGTGTGATTTCTTACACAAATGAGAAAGATTTTTCAGAGTCTGTAT 755

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Db      233 GAGGAGAAAGTNGTGGATTTCCTACACAGTAGAGAAAGATTTCAGAGAGCTGTGNAT 174
QY      756 AAGACACAACTATCTATGGAAGAGAGAGAAATATGGTCAAGAGCAATTTATGGC 815
Db      173 AAGACACAACTATCTATGGAAGAGAGAGAAATATGGTCAAGAGCAATTTATGGC 114
QY      816 TGAGATGAAACATATACATGTGGCTGCTGTGTTTGTAAACCAATGATTAATCTTC 875
Db      113 TGAGATGAAACATATACATGTGGCTGCTGTGTTTGTAAACCAATGATTAATNTTC 54
QY      876 ACTTGAGAAAGCACTTCTAGGAATGTTTAAATAAAGAGTCTTCACCTT 928
Db      53 ACTTGAGAAAGCACTTCTAGGAATGTTTAAATAAAGAGTCTTCACCTT 1

RESULT 7
ADL29442/c
ID      ADL29442 standard; cDNA, 533 BP.
XX
AC      ADL29442;
XX
DT      20-MAY-2004 (first entry)
XX
DE      3' end of a human cDNA molecule SegID 1475.
XX
KW      human; medicine; signal transduction; glycoprotein; transcription;
KM      oligo-capping method; ss.
XX
OS      Homo sapiens.
XX
PN      EP1396543-A2.
XX
PD      10-MAR-2004.
XX
PF      07-JUL-2000; 2003EP-00025638.
XX
PR      08-JUL-1999; 990P-00194486.
PR      11-JAN-2000; 2000JP-00118774.
PR      02-MAY-2000; 2000JP-00183865.
PR      07-JUL-2000; 2000EP-00114089.
XX
PA      (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI      Ota T, Nishikawa T, Isogai T, Hayashi K, Iehi S, Kawai Y;
PI      Wakematsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR      WPI, 2004-204755/20.
XX
PT      New oligonucleotide primers (830 CDNAe) useful for synthesizing full
XX      length human CDNAe.
XX
PS      Disclosure; SEQ ID NO 1475; 1340bp; English.
XX
CC      This invention relates to a novel primers useful for synthesizing full
CC      length cDNA molecules that encode human proteins. Specifically, it refers
CC      to secretory or membrane proteins that are potential therapeutic agents/
CC      target molecules in the field of medicine, and in particular genes
CC      encoding proteins that are associated with signal transduction,
CC      glycoproteins and transcription. The present invention describes a method
CC      for efficiently cloning a full length human cDNA from both the 5' and 3'
CC      ends using the oligo-capping method. This polynucleotide sequence is the
CC      3' end of a full length human cDNA sequence of the invention.
XX
SQ      Sequence 533 BP; 150 A; 103 C; 89 G; 175 T; 0 U; 16 Other;
Query Match 17.5%; Score 476.2; DB 12; Length 533;
Beat Local Similarity 93.4%; Pred. No. 3.4e-107;
Matches 498; Conservative 0; Mismatches 34; Indels 1; Gaps 1;
QY      396 GTCCAGAACTCTCTACAGATGACTTGGTATCAAAACCGGAAATATCTTCTCGAGAG 455
Db      532 GTCCAGAACTCTCTACAGATGACTTGGTATCAAAACCGGAAATATCTTCTCGAGAG 473

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QY      456 CCATGTGGCAGACAGCATTTACAGAAATTTAGATGATGCTGTAATGGGTCTGCATGACA 515
Db      472 CCATGTGGCAGACAGCATTTACAGAAATTTAGATGATGCTGTAAT-GGGTCTGCATGACA 414
QY      516 ATCTTATTAATGACTGAAACCTTTTAAAGATACCTTGCTGTATTTCCAGTTCTATACG 575
Db      413 ATTTTATTAATGACTGAAACCTTTTAAAGAAATCTNGGTGTAAATTTCCAGTTTNAATACG 354
QY      576 TCCCTTAATGAATCCCGTATTAAGGAGAGATTAATGCACTGCTATACCAATGGGCGCC 635
Db      353 TCCCTTAATGAATCCCGTATTAAGGAGAGATTAATGCAATTTTGTATACCAATGGGCGCC 294
QY      636 CTGAACATCCCTCTCCCGAGAAAGACTCCCTTTGCTCCCAACCATCAATGCCCTTA 695
Db      293 ATGAACATCCCTCTCCCGAGAAAGACTCCCTTTGCTCCCAACCATCAATGCCCTTA 234
QY      696 GAGGAGAAAGTCTGTGAATTTCTCTACACAGTAGAGAAAGATTTTTCAGAGTCTGTGAT 755
Db      233 GAGGAGAAAGTNGTGGATTTCCTACACAGTAGAGAAATTTTTCAGAGTCTGTGNAT 174
QY      756 AAGACACAACTATCTATGGAAGAGAGAGAAATATGGTCAAGAGCAATTTATGGC 815
Db      173 AAGACACAACTATCTATGGAAGAGAGAGAAATATGGTCAAGAGCAATTTATGGC 114
QY      816 TGAGATGAAACATATACATGTGGCTGCTGTGTTTGTAAACCAATGATTAATCTTC 875
Db      113 TGAGATGAAACATATACATGTGGCTGCTGTGTTTGTAAACCAATGATTAATNTTC 54
QY      876 ACTTGAGAAAGCACTTCTAGGAATGTTTAAATAAAGAGTCTTCACCTT 928
Db      53 ACTTGAGAAAGCACTTCTAGGAATGTTTAAATAAAGAGTCTTCACCTT 1

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RESULT 8
ADC32380
ID      ADC32380 standard; cDNA, 522 BP.
XX
AC      ADC32380;
XX
DT      18-DEC-2003 (first entry)
XX
DE      Human novel cDNA contig sequence, SEQ ID NO:2462.
XX
KW      Human; diagnostic; drug screening; forensics; gene mapping;
KW      biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW      neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW      ulcers; osteoporosis; autoimmune disease; cancer;
KW      molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW      neuroprotective; anti-inflammatory; anticoagulant; thrombolytic; vulnery;
KW      antileuk; osteopathic; immunosuppressive; antiinflammatory; cyostatic;
KW      gene therapy; chromosome 5; ss.
XX
OS      Homo sapiens.
XX
PN      WO2003029271-A2.
XX
PD      10-APR-2003.
XX
PF      24-SEP-2002; 2002WO-US030474.
PR      24-SEP-2001; 2001US-0324631P.
XX
PA      (HYSE-) HYSEQ INC.
XX
PI      Tang TY, Zhang J, Ren F, Xue AJ, Zhao QH, Wang J, Wehrman T;
PI      Zhou P, Ghoosh M, Wang D, Ma Y, Asundi V, Wang Z, Wang G;
PI      Haley-Vicente D, Dimaac RT;
XX
DR      WPI, 2003-371981/35.
DR      P-PsDB; ADC33147.
XX
PT      New polynucleotide and polypeptide useful for diagnosing, preventing or
XX      treating conditions such as neurodegenerative diseases, anemia, platelet

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OY      2652 CATGCCCTGCAAACTGGGCAATTGATGATTAATGTTATTTTAAATAAATGTTTTTA 2711
        |||||||
DB      66 CATGCCCTGCAAACTGGGCAATTGATGATTAATGTTATTTTAAATAAATGTTTTTA 7
OY      2712 TTCTTT 2717
        ||||||
DB      6 TTCTTT 1
        ||||||

RESULT 10
ACD94489/C
ID      ACD94489 standard; cDNA; 660 BP.
AC      ACD94489;
XX
XX
DT      23-SEP-2003 (first entry)
DE      Human colon cancer cell expressed cDNA #2901.
XX
XX      Open reading frame detection; genome sequencing; colon cancer;
KM      breast cancer; population genome analysis; genetic shift; cancer;
KM      antibiotic resistance; antibiotic non-tolerance; congenital disease;
KM      agriculture; food crop genome; resistance gene; retrovirus;
KM      influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
KM      gene; ss.
XX
XX      Homo sapiens.
OS
XX
XX      US2002155438-A1.
XX
XX      24-OCT-2002.
XX
XX      27-SEP-1999; 99US-00406117.
XX
XX      20-NOV-1998; 98US-00196716.
XX
XX      (SIMP/) SIMPSON A J G.
PA      (NETO/) NETO E D.
PA      (BREN/) BRENTANI R R.
XX
XX      Simpson AJG, Neto ED, Brentani RR;
PI      Simpson AJG, Neto ED, Brentani RR;
XX
XX      WPI; 2003-182626/18.
XX
XX      Determining open reading frames of genome of an organism e.g. a human
PT      suffering from cancer involves use of single oligonucleotide primer at
PT      low stringency for preparing single-stranded cDNA from mRNA of
PT      individual.
XX
XX      Example 9; Page 430; 959pp; English.
XX
XX      The invention describes a method of determining open reading frames in
CC      the genome of organism, comprising contacting mRNA from cell of organism
CC      with a single oligonucleotide primer (I) at low stringency, preparing
CC      single-stranded cDNA by reverse transcribing mRNA with (II), amplifying
CC      cDNA, sequencing the product, and repeating the contacting, preparing
CC      and amplifying steps with different primers and sequencing resulting
CC      nucleic acids. The method is useful for: determining that a known
CC      nucleotide sequence from a genome of an organism corresponds to a
CC      nucleotide sequence of an open reading frame; for preparing a contig,
CC      nucleic acid molecule from a genome of an organism; and for sequencing
CC      all or part of a genome of an organism. mRNA is obtained from mammalian
CC      or human cell which is associated with a pathological condition e.g. a
CC      colon cancer or breast cancer cell. The method is useful for analyses of
CC      populations of subjects and can be used to carry out genetic analyses of
CC      large or small populations. further, it can be used to study living
CC      systems to determine if, e.g. there have been genetic shifts which render
CC      an individual or population more or less likely to be afflicted with
CC      diseases such as cancer, to determine antibiotic resistance or non-
CC      tolerance, and so forth. The method can also be used in the study of
CC      congenital diseases, and the risk of affliction to a fetus, as well as
CC      the study of whether the conditions are likely to be passed to offspring

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CC      through ova or sperm. The analyses for pathological conditions can be
CC      carried out in all animals, plants, birds, fish, etc. Using this method,
CC      in the area of agriculture, for example the genomes of food crops can be
CC      studied to determine if resistance genes are present, defects in plant
CC      genomes can also be studied in this way. Similarly, the method permits
CC      determination of the pathogens which integrate into the genome, such as
CC      retroviruses and other integrating viruses such as influenza virus, have
CC      undergone shifts or mutations, which may require different approaches to
CC      therapy. This method is also applied to eukaryotic pathogens, such as
CC      trypanosomes, different types of Plasmodium, etc. The method essentially
CC      eliminates sequencing of non-coding portions. This sequence represents a
CC      polynucleotide isolated from human colon cancer cell cDNA library
XX
XX      Sequence 660 BP; 180 A; 139 C; 156 G; 180 T; 0 U; 5 Other;
XX
XX      Query Match      5 8%; Score 156.4; DB 10; Length 660;
XX      Best Local Similarity 73.6%; Pred. No. 3.7e-28;
XX      Matches 270; Conservative 0; Mismatches 82; Indels 15; Gaps 5;
OY      2309 TAAAGACATTTTGGCTTAATTTCTTTTCTTATTCCTCCCACTGTAATCCCTACAGTA 2368
        |||||||
DB      538 TAAAGTCTGAGAGCATTTGCTATTTCTTTTCTATCCCACTGTAATCCCTCAGT- 480
OY      2369 CCGGATCTGACACATCTTTTGGACGTTACCTTCAAGCCATGAACCAAAAGCTTCT 2428
        |||||||
DB      479 -CGGATCTGACACATCTT-----GCAGTACCTCTTATAGCCATG-ACCCAAAGTCT 426
OY      2429 ATGAGAGACATGCAAGTATGATCAAGCCCTCATTCGTATGACTTATTAAGAGAGACA 2488
        |||||||
DB      425 AT-AGAGACATGCAAGTATGATCAAGCCCTCATTCGTATGACTTATTAAGAGAGACA 374
OY      2489 TGGTTTCATTGCAATAGTACATTTTCTTACCTTAAAGCTTGAATAGTACTACT 2548
        |||||||
DB      373 TGGTTTCATTGCAATAGTACATTTTCTTACCTTAAAGCTTGAATAGTACTACT 314
OY      2549 CACTTCTCTTTTTCAGTTTCAATATAGTATTCATTTTGGCATTAAGTCTCTGTA 2608
        |||||||
DB      313 CACTTCTCTTTTTCAGTTTCAATATAGTATTCATTTTGGCATTAAGTCTCTGTA 254
OY      2609 AAGCCATTTTATATCTAATTAATAAAGTGAAGTCCCACTCTTCATGCTGCAACTTG 2668
        |||||||
DB      253 AAGCCATGATCTCCGCGACCGGACGACCATTTGGCACCGAATTCGATCCTTAACAAG 194
OY      2669 GGGCAAT 2675
        |||||
DB      193 CGGCAAT 187
        |||||

RESULT 11
AAAX10464/C
ID      AAAX10464 standard; DNA; 104 BP.
XX
XX      AAAX10464;
XX
XX      30-MAR-1999 (first entry)
XX
XX      Human biallelic polymorphic DNA fragment WI-11806.
XX
XX      Polymorphism; biallelic; human; forensic; paternity testing; disease;
KM      detection; phenotypic typing; characteristic; infection; hereditary;
KM      autoimmune disease; cancer; inflammation; drug; therapy; medicament;
XX      treatment; marker; ss.
XX
XX      Homo sapiens.
OS
XX
XX      WO9820165-A2.
XX
XX      14-MAY-1998.
XX
XX      05-NOV-1997; 97WO-US020313.
XX
XX      06-NOV-1996; 96US-0030455P.
XX

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PA (WHEED) WHITEHEAD INST BIOMEDICAL RES.
 XX Lander ES, Wang D, Hudson T;
 XX WPI, 1998-286974/25.
 DR New isolated nucleic acid segments from the human genome - used for
 XX determining polymorphic forms for use in e.g. forensics, paternity
 PT testing or phenotypic typing for disease.
 XX
 PS Claim 1, Page 53; 310pp; English.
 XX
 CC AAX10269-X12937 are human DNA fragments which contain biallelic
 CC polymorphic markers which have been isolated using the primers
 CC represented in AAX09121-X10268. The base occupying the polymorphic site
 CC is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
 CC can be used in methods for determining polymorphic forms in an individual
 CC for use in e.g. forensics, paternity testing or for phenotypic typing for
 CC diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan
 CC syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
 CC familial hypercholesterolemia, polycystic kidney disease, hereditary
 CC spherocytosis, von Willebrand's disease, tuberculous sclerosis, hereditary
 CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
 CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
 CC autoimmune diseases, inflammation, cancer, diseases of the nervous
 CC system, infection by pathogenic microorganisms, and characteristics such
 CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
 CC endurance, fertility, and susceptibility or receptivity to particular
 CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
 CC segments can also be used to produce medicaments for the treatment or
 CC prophylaxis of such diseases
 XX
 SQ Sequence 104 BP; 34 A; 15 C; 23 G; 31 T; 0 U; 1 Other;
 Query Match 3.8%; Score 103.6; DB 2; Length 104;
 Best Local Similarity 99.0%; Pred. No. 1.9e-15;
 Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 2592 CCATATGCTCTCTGTAAGCAATTTATATCTAATAAAGTGAAGTCCACTTT 2651
 DB 104 CCATATGCTCTCTGTAAGCAATTTATATCTAATAAAGTGAAGTCCACTTT 45
 OY 2652 CATGCTGCGCAAACTTGCGGCAATTGATGCTAAATGGTATTTT 2695
 DB 44 CATGCTGCGCAAACTTGCGGCAATTGATGCTAAATGGTATTTT 1
 RESULT 12
 ABN46564/c
 ID ABN46564 standard; DNA; 60 BP.
 AC
 XX ABN46564;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:19312.
 XX
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200210449-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 20-JUL-2001; 2001WO-1B001903.
 XX
 PR 28-JUL-2000; 2000US-0221607P.
 XX
 PR 02-MAY-2001; 2001US-0287724P.
 XX
 PA (COMP-) COMPUGEN INC.
 XX

PI Shoshan A, Maeserman A, Mintz E, Mintz L, Faigler S;
 XX WPI, 2002-257383/30.
 DR
 XX
 PT New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a
 PT genome, useful for detecting tissue-, pathology-, and developmental-
 PT specific genes.
 XX
 PS Example 1, SEQ ID NO 19312; 47pp; English.
 XX
 CC The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
 CC)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises several
 CC oligonucleotides, each capable of hybridizing selectively to a set of
 CC messenger RNAs transcribed from a given transcription unit of the genome,
 CC which encodes one or more messenger RNA splice variants. The
 CC oligonucleotide libraries are useful for detecting mRNAs from a
 CC quantitative sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterizing the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a particular
 CC biological or pathological state, and so allowing the detection of tissue
 CC - and pathology-specific genes such as those genes only expressed in
 CC specific tissue under a specific pathological condition; to detect
 CC developmental specific genes; and to detect RNA transcripts and splice
 CC variants of a transcriptome of a patient suffering from a particular
 CC disorder. ABN2725 to ABN59589 represent oligonucleotide sequences from
 CC rats, humans and mice, which are used in the exemplification of the
 CC present invention. N.B. The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
 XX
 SQ Sequence 60 BP; 24 A; 10 C; 12 G; 14 T; 0 U; 0 Other;
 Query Match 2.1%; Score 58.4; DB 6; Length 60;
 Best Local Similarity 98.3%; Pred. No. 0.00023;
 Matches 59; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 2490 GGTTCATTCATGTCATGTCATTTTCTTACGCTTAAGTTCGATGTAAGTCACTAC 2549
 DB 60 GGTTCATTCATGTCATGTCATTTTCTTACGCTTAAGTTCGATGTAAGTCACTAC 1
 RESULT 13
 ABL32333
 ID ABL32333 standard; DNA; 8895 BP.
 AC
 XX ABL32333;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human immune system associated gene SEQ ID NO: 306.
 XX
 KW Human; immune system disease; cytosine methylation; antiasthmatic;
 KW antiarteriosclerotic; antiangioma; cytosine; monocytic;
 KW neutrophilic; anti-HIV; anticonvulsant; ophthalmologic;
 KW antineoplastic; antiarthritic; antidiabetic; antipsoriatic;
 KW antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
 KW ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200200928-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 02-JUL-2001; 2001WO-EP007537.
 XX

XX	Human; signal transduction associated gene; cytosine methylation state;
XX	Cpg island; signal transduction associated disease; solid tumour; cancer;
KW	antitumour; cytostatic; mutant; ds.
KX	
XX	Homo sapiens.
OS	Synthetic.
XX	
XX	WO200200926-A2.
PN	
XX	
XX	03-JAN-2002.
PD	
XX	
XX	29-JUN-2001; 2001WO-EP007472.
PF	
XX	30-JUN-2000; 2000DE-01032529.
PR	
PR	01-SEP-2000; 2000DE-01043826.
XX	
XX	
PA	(EPIG-) EPIGENOMICS AG.
XX	
PI	Olek A, Piepenbrock C, Berlin K;
XX	
XX	WPI; 2002-147896/19.
DR	

Query Match	1.9%	Score	50.8	DB	6	Length	10543
Best Local Similarity	45.5%	Pred. No.	0.14				
Matches	221	Conservative	0	Mismatches	262	Indels	3
						Gaps	1

OY	2103	GGGAACAAGCAAAAAGTTGGATTCGATTAAGGTATGTGTGACAGAAAGCTTT	2166
Db	2257	GGCGATGATGAGAGAGATTTTGTATTAABAAAATAAAATTAATGATGCTTTATT	3016
OY	2163	ATATATGCTTTATATGAAAAGATATTTTGTATTTGACAGCATTAATTTATTTAATG	2222
Db	3017	TTAATAGGGTGTAAAGATTTAAATGATTTGTATTTAATAGTATATTAATATATATTTAT	3076
OY	2223	CTGTCAATTACACTTAAGTCA CAGGAAAAAATATATACATGCTTACTCAGGCTTCTTAAA	2282
Db	3077	TGTATTTATTTTGAATATTTATTTATTTAAATTTAGGGGTACGCGCTTTTTTTTTTTT	3136
OY	2283	AATATAATTTTATATGAGATCCGTGAGTAAAGCATTTGCTTAATTTCTTTTCTTAAT	2344
Db	3137	TATGTATTTAAAGATTTTATTTTATTTTAAAGAAAATATATGTTTATATTAATTTTAACTT	3198
OY	2343	CCCCACTTGTATATCCCTACACAGTACGGGATCTGCACATCTTTTTCAGATTAACCTC	2402

Db	3197	AGTTTATTTTTTTATTTTTTATTAAGATGAAATATTTTAAATAGTTATTTTAAAT	3256
Qy	2403	TTGATAGCCATGAAACCAAAACGTTTATATGAGAGCATGCAAGTACAGCCCTCAT	2462
Db	3257	TTGATTTTTTAAATATGAAAGTTTTTTTTTAAATTTTAAATATTAATTAAGAGTTGTTA	3316
Qy	2463	CCTGTAGTACTTATTAAGAGAGAGATGTTTTCACTGCATAGTACATTTCTTACCT	2522
Db	3317	TTTTTTAAAGTTTTTATTTTTTTTTTATAGTTATTTTTTATATAGTAA--TTAATTAAGTGT	3373
Qy	2523	TAAAGTTCTGATAGTACCTTACTACTCCTCTTTTCAGTTTTCATATAAGTATTC	2582
Db	3374	TGTTTTTGAATATGATATTTAGATTTTAAATTTTTTGTTTAAAGTTTTTAAATAGTTTTTT	3433
Qy	2583	ATTTTT 2588	
Db	3434	AAAGTT 3439	

Search completed: September 23, 2005, 02:52:42
Job time : 1412 secs

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OM nucleic - nucleic search, using sw model

Run on: September 23, 2005, 02:09:46 ; Search time 445 Seconds
(without alignments)
9990.481 Million cell updates/sec

Title: US-10-617-217A-88

Perfect score: 2717
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 240568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:
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5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	50.8	1.9	1141	US-09-806-708B-22	Sequence 22, Appl
2	50.6	1.9	1141	US-09-806-708B-22	Sequence 22, Appl
3	49.8	1.8	7218	US-08-232-463-14	Sequence 14, Appl
4	48.6	1.8	7218	US-08-232-463-14	Sequence 14, Appl
5	47.8	1.8	55195	US-09-949-016-15854	Sequence 15854, A
6	47.7	1.7	601	US-09-949-016-54021	Sequence 54021, A
7	47.7	1.7	601	US-09-949-016-54022	Sequence 54022, A
8	47.7	1.7	601	US-09-949-016-54022	Sequence 54022, A
9	47.7	1.7	601	US-09-949-016-54022	Sequence 54022, A
10	47.7	1.7	601	US-09-949-016-108655	Sequence 108655, A
11	47.7	1.7	601	US-09-949-016-108655	Sequence 108655, A
12	47.7	1.7	104520	US-09-949-016-108658	Sequence 108658, A
13	47.7	1.7	126029	US-09-949-016-14731	Sequence 14731, A
14	46.6	1.7	601	US-09-949-016-54021	Sequence 54021, A
15	46.6	1.7	601	US-09-949-016-54021	Sequence 54021, A
16	45.4	1.7	601	US-09-949-016-54020	Sequence 54020, A
17	45.4	1.7	601	US-09-949-016-108654	Sequence 108654, A
18	45.2	1.7	19438	US-09-949-016-12699	Sequence 12699, A
19	45.2	1.7	103988	US-09-949-016-12513	Sequence 12513, A
20	45.2	1.7	103988	US-09-949-016-12513	Sequence 12513, A
21	44.8	1.6	45587	US-09-949-016-17050	Sequence 17050, A
22	44.6	1.6	146401	US-09-949-016-15836	Sequence 15836, A
23	44.4	1.6	23501	US-09-949-016-16151	Sequence 16151, A
24	43.6	1.6	15236	US-09-949-016-17517	Sequence 17517, A
25	43.6	1.6	44353	US-09-949-016-16778	Sequence 16778, A
26	43.6	1.6	50381	US-09-949-016-15302	Sequence 15302, A
27	43.6	1.6	58597	US-09-949-016-17122	Sequence 17122, A
				US-09-949-016-13598	Sequence 13598, A

C 28	43	1.6	832	US-09-621-976-2813	Sequence 2813, Ap
29	43	1.6	317366	US-09-949-016-16001	Sequence 16001, A
30	42.8	1.6	1055	US-09-806-708B-23	Sequence 23, Appl
31	42.8	1.6	331814	US-09-949-016-12008	Sequence 12008, A
32	42.8	1.6	331814	US-09-949-016-12008	Sequence 12008, A
33	42.6	1.6	601	US-09-949-016-17056	Sequence 17056, A
34	42.6	1.6	1939	US-07-715-751B-2	Sequence 2, Appl1
35	42.4	1.6	55264	US-09-949-016-15014	Sequence 15014, A
36	42.4	1.6	94755	US-09-949-016-11839	Sequence 11839, A
37	42.4	1.6	119153	US-09-949-016-12378	Sequence 12378, A
38	42.2	1.6	1455	US-09-917-265A-104	Sequence 104, App
39	42.2	1.6	1455	US-09-917-265A-106	Sequence 106, App
40	42.2	1.6	250715	US-09-949-016-13294	Sequence 13294, A
41	42	1.5	152132	US-09-949-016-13845	Sequence 13845, A
42	42	1.5	152145	US-09-949-016-12371	Sequence 12371, A
43	41.8	1.5	1055	US-09-806-708B-23	Sequence 23, Appl
44	41.8	1.5	640681	US-09-790-988-1	Sequence 1, Appl1
45	41.6	1.5	6265	US-09-129-112-3	Sequence 3, Appl1

ALIGNMENTS

```
RESULT 1
US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURES:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.C., L.a., and B.N. FAEI promoters
US-09-806-708B-22

Query Match 1.9%, Score 50.8, DB 4, Length 1141,
Best Local Similarity 10.8%, Pred. No. 0.0012,
Matches 81, Conservative 279, Mismatches 390, Indels 3, Gaps 1;

Cy 945 CACAGAGAAAGTAATTTCTGACGAGCCTATAAAATGTGACTTTTGAATGCTTC 1004
   :::::::::::::::::::::
Db 860 YHHAAKRWMAWMTKTNNNNNNNNNACRNTTWWABKSHWCNNNNNNNNNNNTWC 801

Cy 1005 AGTAACTGACATGTCAGAGTTCAGAGCTTTTCTTCAATTTCTAGTTCATG 1064
   :::::::::::::::::::::
Db 800 HTTANABBCVRANNNNAABMATTCNNWAAATTTHTDCYKRWMTTWMDWTMBT 741

Cy 1065 GATATGAAAAAGAAATTCATTCATTCATTCCTGTGATTTGAACCTTGACAAAACCTGT 1124
   :::::::::::::::::::::
Db 740 TTTATTTSTTMTNNNNNNNNNNMMACTNNNNNNNNKAYAHATNNMGCWNNNTDARFRNTTV 681

Cy 1125 ATGACAGACATTTTAAATATGACAACTTTATTTCTGTAATTTGATCTCAAGG 1184
   :::::::::::::::::::::
Db 680 WRRRWMTNTKRWSTTRRHHTTATNNNNNNNNNNNNNNNSCCTCTRWMTWTMTMGD 621

Cy 1185 ACACAGAAAAAATGCCCCAGAGATCTGATCACTTCTCTGAGGACCTCTCAT 1244
   :::::::::::::::::::::
Db 620 GMTATKKKVRBDITCTVDWADSWVMWYANWMCGRVTTYRNNNTYCKSYAHSYWYNN 561

Cy 1245 GGATGTTGCAATTAAGCACTTGCGGTACTATCAACCAAGAAATTAATGATTCAGAAATAGAAC 1304
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Db 560 AMWYRSASRWSSWABWTRNNMWSGBVWRWAGTWWRHNNNNNTDTRYWMMKMA 501
 Oy 1305 ATTTAGCATGTTAAAGCTTGATGATATATAATCGAAATAGATGGAATGSGAAC 1364
 Db 500 RBTYYDSMCNAKSMRGNMRAKMMWAAANDAGADHDWYNNNTMMRBRAMKMN 441
 Oy 1365 TTTTAAAGAACCAGTCAAAATGATTTTGTGGAATCTGCATTTATTTGAGGATTT 1424
 Db 440 MAMCRALCCNNNNRACVNHGKMRRTKTMKOLACNNNBKMYRVRVAMMTSRDTT 381
 Oy 1425 CCCACACCGATTCACAG---CCCATTTGATAGTGTGATAGGACATTCGGAATG 1481
 Db 380 NTDMMWTSDBWBMHYTVDYTWBRAMNNNNNNNNNBCKTSSMMWMDHNNHTCTGNWTM 321
 Oy 1482 GTGTTCACAGCGTCCCGGCGCTTAAATCTCTCATATTTAGTATTCATTTGATTAAG 1541
 Db 320 GSAYBMAAMSMWAGASNBVTYNNWCMRTYMGKTNNNNNNNNKAYUYRTKVAMCNRYY 261
 Oy 1542 CTTTATTTGACAGAGCTTCAAAAAGCGTATACTGTGAGTGGCCAGATATTCATTTT 1601
 Db 260 YDTAVMTKRYKYCYATVBYWYBMGKHMBMRBRABRSNNMMWVCRAKMYVSMYH 201
 Oy 1602 TAGATCAAAAACCTCTCTTATGAGAGCTTTAAAGTTCCGTACACAAATCTCTCT 1661
 Db 200 AMRYBKABAVGCNNNMKDRMAHHHWCATNNNNMMWYAYMHHHMKKAAVATNNKTABR 141
 Oy 1662 CAGAGATTTTCTCATTTAGTCTTCAAGTA 1694
 Db 140 DDBAHVKTYYWYRDCAMCMMAKAKVRTA 108

RESULT 2

; Sequence 22, Application US/098067088
 ; Patent No. 6784342
 ; GENERAL INFORMATION:
 ; APPLICANT: The University of British Columbia
 ; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
 ; FILE REFERENCE: 4810-58741
 ; CURRENT APPLICATION NUMBER: US/09/806,7088
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: US 60/147,133
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 22
 ; LENGTH: 1141
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; NAME/KEY: Promoter
 ; LOCATION: (1)..(1141)
 ; OTHER INFORMATION: consensus sequence of A.T., L.a., and B.n. FAE1 promoters
 US-09-806-7088-22

Query Match 1.9%; Score 50.6; DB 4; Length 1141;

Best Local Similarity 9.9%; Pred. No. 0.0014; Mismatches 412; Indels 5; Gaps 1;

Matches 79; Conservative 306; Mismatches 412; Indels 5; Gaps 1;
 Oy 1840 AGCCCTTCTGCCATCTGATGAGGAGCATGCTTCACTTGAGATGAGGATGGGGTG 1899
 Db 62 ARMYCKYRWNNKSRMKWYKKMYCBANNTSRYABRABKDKMTAYBMVTMKMGKT 121
 Oy 1900 GAGATGGGTATGATGATGATGAGAAAGCCCTTCCGGATCATGAGATTTGTTCT 1959
 Db 122 GWRHRYWWRMBADTVDDHYYVAMNNAMTTMCMMDKDRRTWMMKNNNATGMDDTKY 181
 Oy 1960 AGTCAATTTCTGCACATGAGATGATGATGAGGAAATGATTAATTAATTAATTAATTA 2019
 Db 182 HMMNNNGBYTYWYRYKTRDRMSKRNMYGBMMKMSYDVTYYWWMWDDCKRKYRW 241
 Oy 2020 TCTGTGAATGAAGGTTGAATGATGATCTTAAAGGCTTTGCTCTATGAGAT 2079

Db 242 VRTGBRYNVVAMBTAHRRRYYNNGTBBAMAYRRRTMNNNNNNNAKAMCKRKYWGMBAB 301
 Oy 2080 GTGAAAA-----CTAGGACCAACAAAAGGAACAGAAAAGTTTGATTCGATTA 2134
 Db 302 VNSCTTWSKXTTYKRSVCMVNCRADPDANDHMKWKSAAAGYVNNNNNNNTYTKAR 361
 Oy 2135 GTGATATGTAATAGTGCAGAGGCTTTATATATGCTTATATGATAAGATAATTTTTGT 2194
 Db 362 HBAAWDMVMSAKWMAAHHYRSKKTBYKRTMYNNNNNTTMMKEMWVYKMDMDW 421
 Oy 2195 ATATGACAGATATATTAATTTTAAATGCTGTCATTAACATTAAGATCAAGAAAAAA 2254
 Db 422 BGTNNNNNGRTYYGWTYKNNKMTYYKAKYNNCKEABMDHKTCTHNNTYMMKMYNN 481
 Oy 2255 TATACATGCTTACGACGCTTCTTAAAAAATAATTTTAAAGAGATCTTGATTAAGA 2314
 Db 482 CYWKSMTNGSHRBAALVYTWYMMWRYYAANNNDYMKACTWYKYVCSKMNYYA 541
 Oy 2315 CATTTGCTTAATTTCTTTTCTTATTCCTTGTATATCCCTGATATCCCTACAGTACGGGA 2374
 Db 542 AMYTKSMYTSRYRYRMKTNNSMRSDTSMGBANNYABABHYGYKMTREMBSHTWB 601
 Oy 2375 TCTGCACACATCTTTTGGAGTACCTCTTCATAGCCATGACCAAAAAGTTTATGAG 2434
 Db 602 HBRAGAHHYMBWYBAKCHCMKAMYAKKYAGAGSSNNNNNNNNNNNNNNNNATCARD 661
 Oy 2435 AGCATGACAGTAATCAAGCTCTATCTGTGATTAATTAAGAGAGAGATGTTT 2494
 Db 662 YYASRYVAMANAAYYKYBAANNAVYTHANNMGCMNATDTIRTKNNNNNNNAGTWK 721
 Oy 2495 TCATGATAGTGCATTTTCTTACCTTAAGCTTGAATGATGATGATGATGATGATGATG 2554
 Db 722 NNNNNNAKMSAAKGYAAAKAKGABRWANKRABGMHDAABTTDKNNNGAYTKAT 781
 Oy 2555 TCTTTTCAAGTTTCATTAATGATGATGATTTTGGCATTAAGCTTCCGTGAAGCA 2614
 Db 782 TTNNNNYRGVYTTAARDGANNNNNNNNNNNNNNNNNGSDMWYTWAAVAGYNNNNNN 841
 Oy 2615 ATTATATCTAATAAACAAT 2636
 Db 842 NNAAYAWTKMYTTTDDRMB 863

RESULT 3

; Sequence 14, Application US/08232463
 ; Patent No. 3670367

; GENERAL INFORMATION:
 ; APPLICANT: DORNER, F.
 ; APPLICANT: SCHEIFLINGER, F.
 ; APPLICANT: FALKNER, F. G.
 ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 1800 Diagonal Road, Suite 500
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22313-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/232,463
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/935,313
 ; FILING DATE:
 ; APPLICATION NUMBER: EP 91 114 300.6

US-08-232-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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RESULT 5
US-09-949-016--15854/C
: Sequence 15854, Application US/09949016
: Patent No. 681239
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CL001307
: CURRENT APPLICATION NUMBER: US/09/949,016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498

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;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 15854
;; LENGTH: 55195
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-15854

Query Match 1.8%; Score 47.8; DB 4; Length 55195;
Best Local Similarity 53.5%; Pred. No. 0.085;
Matches 100; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

Oy 2084 AAAAGTACGACCCAAAGGAGCAAGCAAAAGTTGGATTCGATTAAGTATGT 2143
Db 19373 AAAAGGACGAGAAAGATGAAAAAGAACAAAGTTAAATGGACAAAGAGAAATTA 19314
Oy 2144 AATAGTTCAGAGGCTTTATATATGCTTATTAATGAAAGATTTTGTATATTGACA 2203
Db 19313 CTAACCTGATGTAGATGTAATTCACCTATTTAACTATTCATGCAATGCAATGCGTTT 19254
Oy 2204 GCATTAATTTATTTATGCTGTCATTCACCTTAAGTCAGAGAAATATATACATGC 2263
Db 19253 GAACATCTCAATTTAAAGCTCAGATAATTTAAAGATATATCTACAAATTTAAAAAGA 19194
Oy 2264 TTAATCA 2270
Db 19193 TATATCA 19187

RESULT 6
US-09-949-016-54021
;; Sequence 54021, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; FILE REFERENCE: C1001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 54021
;; LENGTH: 601
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-54021

Query Match 1.7%; Score 47; DB 4; Length 601;
Best Local Similarity 51.7%; Pred. No. 0.0095;
Matches 107; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Oy 2130 ATAAAGTATATGTAATGTTGCAGAGGCTTATATATGCTTATTAAGAAAAGTATTT 2189
Db 165 AT 224
Oy 2190 TTGATATATGACGATTAATTTATTTAATGCTGATTAACCTTAAGTCACAGAA 2249
Db 225 TACAT 284
Oy 2250 AAAATATATACATGCTTACTCAGGCTTCTTAAAAATATTTTATATAGATCCCTGAGT 2309
Db 285 TATATAAT 344
Oy 2310 AAAGACATTTGCTTAAATTTCTTTT 2336

Db 345 AAAT 371

RESULT 7
US-09-949-016-54022
;; Sequence 54022, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; FILE REFERENCE: C1001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 54022
;; LENGTH: 601
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-54022

Query Match 1.7%; Score 47; DB 4; Length 601;
Best Local Similarity 51.7%; Pred. No. 0.0095;
Matches 107; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Oy 2130 ATAAAGTATATGTAATGTTGCAGAGGCTTATATATGCTTATTAAGAAAAGTATTT 2189
Db 160 AT 219
Oy 2190 TTGATATATGACGATTAATTTATTTAATGCTGTCATTCACCTTAAGTCACAGAA 2249
Db 220 TACAT 279
Oy 2250 AAAATATATACATGCTTACTCAGGCTTCTTAAAAATATTTTATATAGATCCCTGAGT 2309
Db 280 TATATAAT 339
Oy 2310 AAAGACATTTGCTTAAATTTCTTTT 2336
Db 340 AAAT 366

RESULT 8
US-09-949-016-54024
;; Sequence 54024, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; FILE REFERENCE: C1001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 54024
;; LENGTH: 601
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-54024

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Query Match 1.7%; Score 47; DB 4; Length 601;
Best Local Similarity 51.7%; Pred. No. 0.0095;
Matches 107; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 2130 ATAAAGTATGTAATAGTTCGAGAGGCTTTATATATGCTTATATGAAAAGATATTT 2189
Db 95 ATATATATATAATATATATAATATAATAATATATAATATAATATAATATAATATA 154
Qy 2190 TTGTATATGACAGCATATTTTATTTTAAATGCTGCTTACACTTAAAGTCACAGAA 2249
Db 155 TACATATATAATATATAATAATAATAATAATAATAATAATAATAATAATAATA 214
Qy 2250 AAAAATATACATGCTTACTCAGGCTTCTTAAATAATTTTATATAGATCCTTGACT 2309
Db 215 TATATAAATATATATAATAATAATAATAATAATAATAATAATAATAATAATA 274
Qy 2310 AAAGCATTTTGCTTAATTTCTTTT 2336
Db 275 AAATATATATATATATATTTT 301

RESULT 9
US-09-949-016-108655
; Sequence 108655, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108655
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-108655

Query Match 1.7%; Score 47; DB 4; Length 601;
Best Local Similarity 51.7%; Pred. No. 0.0095;
Matches 107; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 2130 ATAAAGTATGTAATAGTTCGAGAGGCTTTATATATGCTTATATGAAAAGATATTT 2189
Db 165 ATATATATAAATATATATAATAATAATAATAATAATAATAATAATAATAATA 224
Qy 2190 TTGTATATGACAGCATATTTTATTTTAAATGCTGCTTACACTTAAAGTCACAGAA 2249
Db 225 TACATATATAATATATAATAATAATAATAATAATAATAATAATAATAATAATA 284
Qy 2250 AAAAATATACATGCTTACTCAGGCTTCTTAAATAATTTTATATAGATCCTTGACT 2309
Db 285 TATATAAATATATATAATAATAATAATAATAATAATAATAATAATAATAATA 344
Qy 2310 AAAGCATTTTGCTTAATTTCTTTT 2336
Db 345 AAATATATATATATATATTTT 371

RESULT 10
US-09-949-016-108656
; Sequence 108656, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
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; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108656
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-108656

Query Match 1.7%; Score 47; DB 4; Length 601;
Best Local Similarity 51.7%; Pred. No. 0.0095;
Matches 107; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 2130 ATAAAGTATGTAATAGTTCGAGAGGCTTTATATATGCTTATATGAAAAGATATTT 2189
Db 160 ATATATATAAATATATATAATAATAATAATAATAATAATAATAATAATAATA 219
Qy 2190 TTGTATATGACAGCATATTTTATTTTAAATGCTGCTTACACTTAAAGTCACAGAA 2249
Db 220 TACATATATAATATATAATAATAATAATAATAATAATAATAATAATAATAATA 279
Qy 2250 AAAAATATACATGCTTACTCAGGCTTCTTAAATAATTTTATATAGATCCTTGACT 2309
Db 280 TATATAAATATATATAATAATAATAATAATAATAATAATAATAATAATAATA 339
Qy 2310 AAAGCATTTTGCTTAATTTCTTTT 2336
Db 340 AAATATATATATATATATTTT 366

RESULT 11
US-09-949-016-108658
; Sequence 108658, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108658
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-108658

Query Match 1.7%; Score 47; DB 4; Length 601;
Best Local Similarity 51.7%; Pred. No. 0.0095;
Matches 107; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 2130 ATAAAGTATGTAATAGTTCGAGAGGCTTTATATATGCTTATATGAAAAGATATTT 2189
Db 95 ATATATATAAATATATATAATAATAATAATAATAATAATAATAATAATAATA 154
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[illegible]

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RESULT 15
US-09-949-016-108657
; Sequence 108657, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108657
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-108657

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[illegible]

Search completed: September 23, 2005, 08:36:39
Job time : 449 secs